



results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057859611-03868-12851

Query= SEQID28
(9 letters)

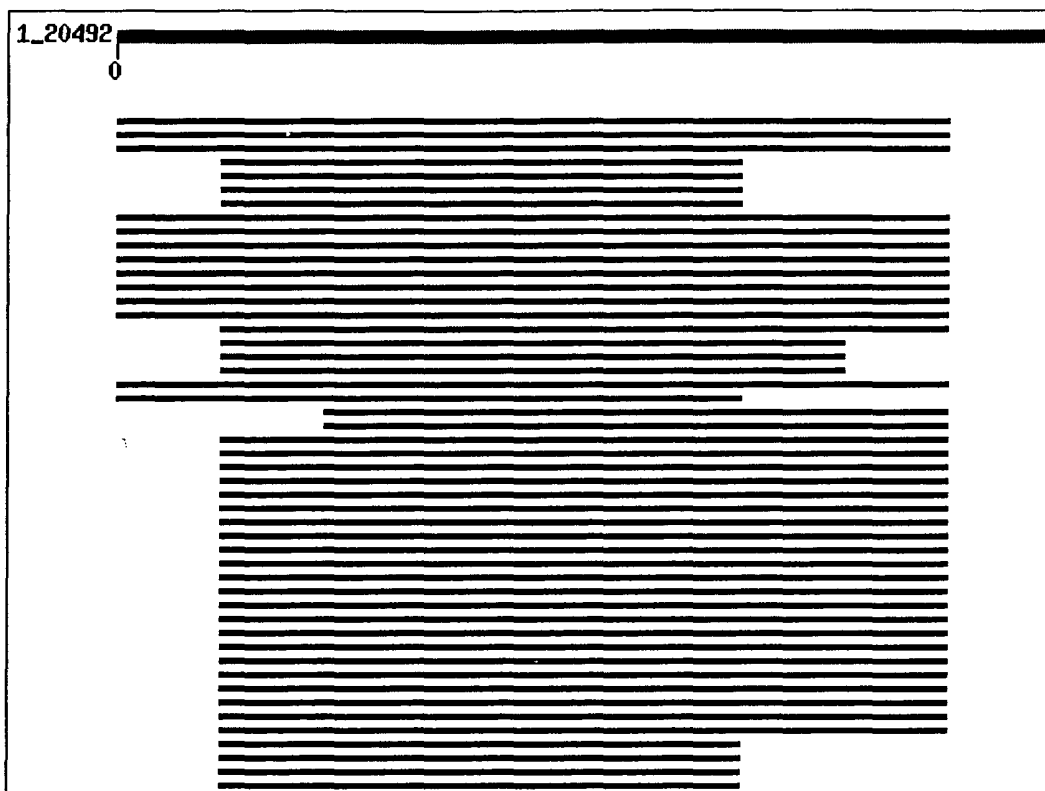
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 128 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

	Score (bits)	E Value	
gi 21355617 ref NP_651115.1 CG10873-PA [Drosophila melanog...	34	0.22	L
gi 25009887 gb AAN71112.1 AT28346p [Drosophila melanogaster]	34	0.22	
gi 31207283 ref XP_312608.1 ENSANGP00000014785 [Anopheles ...	31	1.8	
gi 1709335 sp P21783 NOTC_XENLA Neurogenic locus notch prot...	24	194	
gi 18859115 ref NP_571516.1 notch homolog 1a; neurogenic 1...	24	194	L
gi 27675874 ref XP_228125.1 similar to 40kDa ribosomal pro...	24	194	L
gi 104252 pir A35844 Xotch protein - African clawed frog	24	194	
gi 9626079 ref NP_040318.1 Non-capsid protein [Parvovirus ...	23	468	
gi 22966887 ref ZP_00014482.1 hypothetical protein [Rhodos...	23	468	
gi 22137819 gb AAM93277.1 AF332883_1 nonstructural protein ...	23	468	
gi 8928081 sp Q9ZA11 DHAL_RHORU Aldehyde dehydrogenase >gi ...	23	468	
gi 21238945 dbj BAB96577.1 aldehyde dehydrogenase [Cytopha...	23	468	
gi 23113187 ref ZP_00098587.1 hypothetical protein [Desulf...	23	468	
gi 22137816 gb AAM93275.1 AF332882_1 nonstructural protein ...	23	468	
gi 3033510 gb AAC40695.1 nonstructural protein [Kilham rat...	23	468	
gi 1711120 gb AAB38326.1 non-capsid protein [Kilham rat vi...	23	468	
gi 22137811 gb AAM93272.1 AF321230_1 nonstructural protein ...	23	468	
gi 22137822 gb AAM93279.1 AF332884_1 nonstructural protein ...	23	468	
gi 29823071 ref NP_821154.1 Nonstructural protein NS1 [LuI...	23	468	
gi 18150104 dbj BAB83667.1 insulin receptor [Paralichthys ...	22	843	
gi 31205321 ref XP_311609.1 ENSANGP00000016117 [Anopheles ...	22	843	
gi 23867780 dbj BAC21014.1 claudin4L2 [Xenopus laevis]	22	843	
gi 12848262 dbj BAB27889.1 unnamed protein product [Mus mu...	22	843	L
gi 3695096 gb AAC62642.1 DN p63 gamma [Mus musculus]	22	1131	L
gi 13751181 emb CAC37102.1 DN KET gamma protein [Rattus no...	22	1131	L

gi 13751173 emb CAC37098.1	TA1 KET alpha protein [Rattus n...	22	1131	L
gi 13626617 sp Q9TV36 FBN1_PIG	Fibrillin 1 precursor >gi 57...	22	1131	
gi 3688648 gb AAC62317.1	mutant fibrillin-1 [Mus musculus]	22	1131	L
gi 20428532 gb AAK81886.1	DN p73 gamma [Homo sapiens]	22	1131	L
gi 1813455 gb AAB41833.1	p53	22	1131	
gi 19909983 dbj BAB87245.1	deltaN p73 beta [Homo sapiens] ...	22	1131	L
gi 7248451 gb AAF43492.1	p51 isoform delNbeta [Homo sapiens]	22	1131	
gi 642072 gb AAA61825.1	fibrillin-1	22	1131	L
gi 13929178 ref NP_114013.1	fibrillin-1 [Rattus norvegicus...	22	1131	L
gi 20892181 ref XP_147232.1	transformation related protein...	22	1131	L
gi 3695094 gb AAC62641.1	TA*p63 alpha [Mus musculus]	22	1131	L
gi 12060406 dbj BAB20591.1	delta N p73L [Homo sapiens]	22	1131	
gi 4803651 emb CAA72225.1	P73 splice variant [Cercopithec...	22	1131	
gi 13751179 emb CAC37101.1	TA2 KET gamma protein [Rattus n...	22	1131	L
gi 15072750 emb CAC48053.1	p63 delta [Homo sapiens]	22	1131	
gi 29470179 gb AAO74632.1	p73 [Danio rerio]	22	1131	
gi 2581764 gb AAB82420.1	p53 [Cricetulus griseus]	22	1131	
gi 24430141 ref NP_000129.2	fibrillin 1 [Homo sapiens]	22	1131	L
gi 8217484 emb CAB92742.1	dJ1092A11.2 (tumor protein p73) ...	22	1131	
gi 2370178 emb CAA72221.1	second splice variant [Homo sapi...	22	1131	L
gi 15678984 ref NP_276101.1	conserved protein [Methanother...	22	1131	
gi 21264484 sp P79820 P53_ORYLA	Cellular tumor antigen p53 ...	22	1131	
gi 1184759 gb AAA87577.1	p53 tumor suppressor homolog	22	1131	
gi 1184757 gb AAA87576.1	p53 tumor suppressor homolog	22	1131	
gi 7248450 gb AAF43491.1	p51 isoform delNalpha [Homo sapiens]	22	1131	
gi 7459676 pir A47221	fibrillin 1 precursor - human (fragm...	22	1131	
gi 7248447 gb AAF43488.1	p51 isoform TAp63beta [Homo sapiens]	22	1131	
gi 3273745 gb AAC24830.1	p53 homolog [Homo sapiens]	22	1131	L
gi 473579 gb AAB41344.1	tumor supressor p53 [Mesocricetus ...	22	1131	
gi 27527178 emb CAD10682.1	p53 protein [Monodelphis domest...	22	1131	
gi 12024746 gb AAG45609.1	TA p63 gamma [Homo sapiens]	22	1131	
gi 3695098 gb AAC62643.1	DN p63 beta [Mus musculus]	22	1131	L
gi 4689086 gb AAD27752.1 AF043641_1	p73 [Barbus barbus]	22	1131	
gi 6755883 ref NP_035771.1	transformation related protein ...	22	1131	L
gi 1244762 gb AAA98563.1	p53 tumor suppressor homolog	22	1131	
gi 13751187 emb CAC37105.1	DN KET beta protein [Rattus nor...	22	1131	L
gi 13751175 emb CAC37099.1	DN KET alpha protein [Rattus no...	22	1131	L
gi 17554334 ref NP_498645.1	MUscle Positioning 4, transmem...	22	1131	L
gi 23308709 ref NP_694518.1	deltaNp63 isoform alpha 1; tum...	22	1131	L
gi 26339452 dbj BAC33397.1	unnamed protein product [Mus mu...	22	1131	
gi 23308711 ref NP_694519.1	deltaNp63 isoform gamma; tumor...	22	1131	L
gi 3695082 gb AAC62635.1	TA p63 alpha [Homo sapiens]	22	1131	L
gi 1698502 gb AAC60146.1	p53 [Oryzias latipes] >gi 1208249...	22	1131	
gi 20850793 ref XP_131858.1	transformation related protein...	22	1131	L
gi 13195250 gb AAK15622.1 AF314148_1	p63 DNA binding protei...	22	1131	
gi 14579227 gb AAK69172.1 AF289202_1	transmembrane matrix r...	22	1131	L
gi 3510328 dbj BAA32592.1	p51A [Homo sapiens] >gi 3695078 ...	22	1131	L
gi 13751185 emb CAC37104.1	TA1 KET beta protein [Rattus no...	22	1131	L
gi 451931 gb AAA37086.1	tumor supressor protein [Mesocrice...	22	1131	
gi 1813453 gb AAB41832.1	p53	22	1131	
gi 2494284 sp Q61554 FBN1_MOUSE	Fibrillin 1 precursor >gi 1...	22	1131	L

gi 3695080 gb AAC62634.1 	DN p63 gamma [Homo sapiens]	>gi 7...	22	1131	L
gi 1813451 gb AAB41831.1 	p53		22	1131	
gi 25395876 pir F88508	protein H14A12.6 [imported] - Caeno...		22	1131	
gi 3970717 emb CAA76562.1 	KET protein [Homo sapiens]		22	1131	L
gi 23308685 ref NP_689454.1 	deltaNp63 isoform alpha 2; tum...		22	1131	L
gi 3445484 dbj BAA32433.1 	p73H [Homo sapiens]		22	1131	L
gi 7689271 gb AAF67733.1 AF253323_1	p53 tumor suppressor-li...		22	1131	
gi 6679759 ref NP_032019.1 	fibrillin 1; tight skin [Mus mu...		22	1131	L
gi 17985367 gb AAL50211.1 	tumor protein [Canis familiaris]		22	1131	
gi 31543818 ref NP_003713.3 	tumor protein p73-like; tumor ...		22	1131	L
gi 19909981 dbj BAB87244.1 	deltaN p73 alpha [Homo sapiens]...		22	1131	L
gi 4101546 gb AAD01196.1 	tumor suppressor protein p53 [Ory...		22	1131	
gi 1813457 gb AAB41834.1 	p53		22	1131	
gi 1244764 gb AAA98564.1 	p53 tumor suppressor homolog		22	1131	
gi 7440008 pir JC6176	tumor suppressor protein p53 - Chine...		22	1131	
gi 12856636 dbj BAB30732.1 	unnamed protein product [Mus mu...		22	1131	L
gi 19850152 gb AAL99584.1 AF285104_1	p53-like transcription...		22	1131	
gi 7320915 emb CAB81954.1 	P73 delta-N protein [Mus musculus]		22	1131	L
gi 129370 sp Q00366 P53_MESAU	Cellular tumor antigen p53 (T...		22	1131	
gi 7689273 gb AAF67734.1 AF253324_1	p73-like protein [Mya a...		22	1131	
gi 3695088 gb AAC62638.1 	DN p63 beta [Homo sapiens]	>gi 12...	22	1131	L
gi 27806637 ref NP_776478.1 	fibrillin 1 [Bos taurus]	>gi 1...	22	1131	L
gi 2370177 emb CAA72219.1 	first splice variant [Homo sapiens]		22	1131	L
gi 28487571 ref XP_192917.2 	fibrillin 1 [Mus musculus]		22	1131	L

Alignments

☐ [>gi|21355617|ref|NP_651115.1|](#) [L](#) CG10873-PA [Drosophila melanogaster]
[gi|7211767|gb|AAF40427.1|AF224713_1](#) [L](#) transcription factor p53 [Drosophila melano
[gi|7211769|gb|AAF40428.1|AF224714_1](#) [L](#) transcription factor p53 [Drosophila melano
[gi|7381624|gb|AAF61572.1|AF244918_1](#) [L](#) p53 tumor suppressor-like protein [Drosophi
[gi|8272608|gb|AAF74277.1|AF250918_1](#) [L](#) transcription factor [Drosophila melanogast
[gi|8453176|gb|AAF75270.1|AF263722_1](#) [L](#) transcription factor p53 [Drosophila melano
[gi|10726710|gb|AAF56087.2|](#) [L](#) CG10873-PA [Drosophila melanogaster]
[gi|17861528|gb|AAL39241.1|](#) [L](#) GH11591p [Drosophila melanogaster]
[gi|18032162|gb|AAL56639.1|AF192555_1](#) p53-like regulator of apoptosis and cell cyc
 melanogaster]
 Length = 385

Score = 34.1 bits (73), Expect = 0.22
 Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 KICTCPKRD 9
 KICTCPKRD
 Sbjct: 259 KICTCPKRD 267

┌>gi|25009887|gb|AAN71112.1| AT28346p [Drosophila melanogaster]
Length = 519

Score = 34.1 bits (73), Expect = 0.22
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 KICTCPKRD 9
KICTCPKRD
Sbjct: 393 KICTCPKRD 401

┌>gi|31207283|ref|XP_312608.1| ENSANGP00000014785 [Anopheles gambiae]
gi|21295812|gb|EAA07957.1| ENSANGP00000014785 [Anopheles gambiae str. PEST]
Length = 338

Score = 31.2 bits (66), Expect = 1.8
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 1 KICTCPKRD 9
KIC+CPKRD
Sbjct: 309 KICSCPARD 317

┌>gi|1709335|sp|P21783|NOTC_XENLA Neurogenic locus notch protein homolog precursor
gi|1364263|gb|AAB02039.1| Xotch protein
Length = 2524

Score = 24.4 bits (50), Expect = 194
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7
ICTCPK
Sbjct: 625 ICTCPK 630

Score = 21.4 bits (43), Expect = 1518
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICTCP 6
ICTCP
Sbjct: 396 ICTCP 400

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 1044 CTCP 1047

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 2 ICTC 5
ICTC
Sbjct: 775 ICTC 778

gi|18859115|ref|NP_571516.1| **L** notch homolog 1a; neurogenic locus notch homolog
rerio]
gi|1171748|sp|P46530|NTC1_BRARE Neurogenic locus notch homolog protein 1 precursor
gi|630926|pir|S42612 transmembrane protein precursor - zebra fish
gi|433867|emb|CAA48831.1| **L** transmembrane protein-precursor [Danio rerio]
Length = 2437

Score = 24.4 bits (50), Expect = 194
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7
ICTCPK
Sbjct: 624 ICTCPK 629

Score = 21.4 bits (43), Expect = 1518
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICTCP 6
ICTCP
Sbjct: 396 ICTCP 400

Score = 21.4 bits (43), Expect = 1518
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICTCP 6
ICTCP
Sbjct: 162 ICTCP 166

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 1043 CTCP 1046

gi|27675874|ref|XP_228125.1| **L** similar to 40kDa ribosomal protein [Rattus norvegicus]
Length = 310

Score = 24.4 bits (50), Expect = 194
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7
ICTCPK
Sbjct: 188 ICTCPK 193

┌>gi|104252|pir|A35844 Xotch protein - African clawed frog
Length = 2524

Score = 24.4 bits (50), Expect = 194
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7
ICTCPK
Sbjct: 626 ICTCPK 631

Score = 21.4 bits (43), Expect = 1518
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICTCP 6
ICTCP
Sbjct: 397 ICTCP 401

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 1045 CTCP 1048

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 2 ICTC 5
ICTC
Sbjct: 776 ICTC 779

┌>gi|9626079|ref|NP_040318.1| Non-capsid protein [Parvovirus H1]
gi|138882|sp|P03133|VNCS_PAVHH NONCAPSID PROTEIN NS-1 (NONSTRUCTURAL PROTEIN NS1)
gi|73528|pir|UYPVV1 noncapsid protein NS1 - parvovirus H1
gi|60994|emb|CAA25689.1| Non-capsid protein [Parvovirus H1]
Length = 672

Score = 23.1 bits (47), Expect = 468
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9
KICT P RD
Sbjct: 216 KICTSPPRD 224

┌>gi|22966887|ref|ZP_00014482.1| hypothetical protein [Rhodospirillum rubrum]
Length = 337

Score = 23.1 bits (47), Expect = 468
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 ICTCPKR 8
ICTCP R
Sbjct: 131 ICTCPSR 137

┌>gi|22137819|gb|AAM93277.1|AF332883_1 nonstructural protein 1 [rat minute virus
Length = 672

Score = 23.1 bits (47), Expect = 468
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9
KICT P RD
Sbjct: 216 KICTSPPRD 224

┌>gi|8928081|sp|Q9ZA11|DHAL_RHORU Aldehyde dehydrogenase
gi|4579692|dbj|BAA75070.1| aldehyde dehydrogenase [Rhodospirillum rubrum]
Length = 506

Score = 23.1 bits (47), Expect = 468
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 ICTCPKR 8
ICTCP R
Sbjct: 300 ICTCPSR 306

┌>gi|21238945|dbj|BAB96577.1| aldehyde dehydrogenase [Cytophaga sp. KUC-1]
Length = 501

Score = 23.1 bits (47), Expect = 468
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 ICTCPKR 8
ICTCP R
Sbjct: 295 ICTCPSR 301

┌>gi|23113187|ref|ZP_00098587.1| hypothetical protein [Desulfitobacterium hafnien
Length = 590

Score = 23.1 bits (47), Expect = 468
Identities = 7/9 (77%), Positives = 7/9 (77%), Gaps = 1/9 (11%)

Query: 2 ICT-CPKRD 9
IC CPKRD
Sbjct: 78 ICNNCPKRD 86

┌>gi|22137816|gb|AAM93275.1|AF332882_1 nonstructural protein 1 [rat minute virus]
Length = 672

Score = 23.1 bits (47), Expect = 468
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9
KICT P RD
Sbjct: 216 KICTSPPRD 224

┌>gi|3033510|gb|AAC40695.1| nonstructural protein [Kilham rat virus]
Length = 665

Score = 23.1 bits (47), Expect = 468
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9
KICT P RD
Sbjct: 209 KICTSPPRD 217

┌>gi|1711120|gb|AAB38326.1| non-capsid protein [Kilham rat virus]
Length = 672

Score = 23.1 bits (47), Expect = 468
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9
KICT P RD
Sbjct: 216 KICTSPPRD 224

┌>gi|22137811|gb|AAM93272.1|AF321230_1 nonstructural protein 1 [Kilham rat virus]
Length = 672

Score = 23.1 bits (47), Expect = 468
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9
KICT P RD
Sbjct: 216 KICTSPPRD 224

┌>gi|22137822|gb|AAM93279.1|AF332884_1 nonstructural protein 1 [rat minute virus]
Length = 672

Score = 23.1 bits (47), Expect = 468
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9
KICT P RD
Sbjct: 216 KICTSPPRD 224

gi|29823071|ref|NP_821154.1| Nonstructural protein NS1 [LuIII virus]
gi|549392|sp|P36311|VNCS_PAVL3 NONCAPSID PROTEIN NS-1 (NONSTRUCTURAL PROTEIN NS1)
gi|476350|pir|A44276 noncapsid protein NS1 - parvovirus LuIII
 Length = 668

Score = 23.1 bits (47), Expect = 468
 Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9
 KICT P RD
 Sbjct: 216 KICTSPPRD 224

gi|18150104|dbj|BAB83667.1| insulin receptor [Paralichthys olivaceus]
 Length = 1369

Score = 22.3 bits (45), Expect = 843
 Identities = 6/9 (66%), Positives = 7/9 (77%)

Query: 1 KICTCPKRD 9
 K+C CPK D
 Sbjct: 705 KVCACPKTD 713

Score = 18.0 bits (35), Expect = 15950
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 2 ICTC 5
 ICTC
 Sbjct: 17 ICTC 20

gi|31205321|ref|XP_311609.1| ENSANGP00000016117 [Anopheles gambiae]
gi|30177715|gb|EAA07139.2| ENSANGP00000016117 [Anopheles gambiae str. PEST]
 Length = 261

Score = 22.3 bits (45), Expect = 843
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 KICTCPK 7
 KICTC K
 Sbjct: 223 KICTCTK 229

gi|23867780|dbj|BAC21014.1| claudin4L2 [Xenopus laevis]
 Length = 213

Score = 22.3 bits (45), Expect = 843
 Identities = 5/7 (71%), Positives = 7/7 (100%)

Query: 3 CTCPKRD 9
 C+CPKR+
 Sbjct: 183 CSCPKRE 189

┌>gi|12848262|dbj|BAB27889.1| ┐ unnamed protein product [Mus musculus]
Length = 301

Score = 22.3 bits (45), Expect = 843
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 3 CTCPKRD 9
CTCP RD
Sbjct: 16 CTCPPRD 22

┌>gi|3695096|gb|AAC62642.1| ┐ DN p63 gamma [Mus musculus]
Length = 389

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 250 ICACPGRD 257

┌>gi|13751181|emb|CAC37102.1| ┐ DN KET gamma protein [Rattus norvegicus]
Length = 393

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 250 ICACPGRD 257

┌>gi|13751173|emb|CAC37098.1| ┐ TA1 KET alpha protein [Rattus norvegicus]
Length = 663

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 327 ICACPGRD 334

┌>gi|13626617|sp|Q9TV36|FBN1_PIG Fibrillin 1 precursor
gi|5739075|gb|AAD50328.1|AF073800_1 fibrillin-1 precursor [Sus scrofa]
Length = 2871

Score = 21.8 bits (44), Expect = 1131
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7
+CTCPK
Sbjct: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 100 CTCP 103

 >gi|3688648|gb|AAC62317.1|  mutant fibrillin-1 [Mus musculus]
Length = 3857

Score = 21.8 bits (44), Expect = 1131
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7
+CTCPK
Sbjct: 1775 VCTCPK 1780

Score = 21.8 bits (44), Expect = 1131
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7
+CTCPK
Sbjct: 791 VCTCPK 796


Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 100 CTCP 103

 >gi|20428532|gb|AAK81886.1|  DN p73 gamma [Homo sapiens]
Length = 426

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 245 ICACPGRD 252

 >gi|1813455|gb|AAB41833.1| p53
Length = 238

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 167 ICACPGRD 174

┌>gi|19909983|dbj|BAB87245.1| **L** deltaN p73 beta [Homo sapiens]
gi|20428530|gb|AAK81885.1| **L** DN p73 beta [Homo sapiens]
Length = 450

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 245 ICACPGRD 252

┌>gi|7248451|gb|AAF43492.1| p51 isoform delNbeta [Homo sapiens]
Length = 461

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 250 ICACPGRD 257

┌>gi|642072|gb|AAA61825.1| **L** fibrillin-1
Length = 1095

Score = 21.8 bits (44), Expect = 1131
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7
+CTCPK
Sbjct: 766 VCTCPK 771

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 75 CTCP 78

┌>gi|13929178|ref|NP_114013.1| **L** fibrillin-1 [Rattus norvegicus]
gi|4959650|gb|AAD34438.1| **L** fibrillin-1 [Rattus norvegicus]



Length = 2872

Score = 21.8 bits (44), Expect = 1131
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7
+CTCPK
Sbjct: 790 VCTCPK 795

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 100 CTCP 103

 >[gi|20892181|ref|XP_147232.1|](#)  transformation related protein 63 [Mus musculus]
Length = 465


Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 129 ICACPGRD 136

 >[gi|3695094|gb|AAC62641.1|](#)  TA*p63 alpha [Mus musculus]
Length = 680


Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 344 ICACPGRD 351

 >[gi|12060406|dbj|BAB20591.1|](#) delta N p73L [Homo sapiens]
Length = 501

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 165 ICACPGRD 172

 >[gi|4803651|emb|CAA72225.1|](#) P73 splice variant [Cercopithecus aethiops]
Length = 499

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 294 ICACPGRD 301

┌>gi|13751179|emb|CAC37101.1| ─ TA2 KET gamma protein [Rattus norvegicus]
Length = 487

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 344 ICACPGRD 351

┌>gi|15072750|emb|CAC48053.1| p63 delta [Homo sapiens]
Length = 232

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 192 ICACPGRD 199

┌>gi|29470179|gb|AA074632.1| p73 [Danio rerio]
Length = 640

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 301 ICACPGRD 308

┌>gi|2581764|gb|AAB82420.1| p53 [Cricetulus griseus]
Length = 205

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 149 ICACPGRD 156

┌>gi|24430141|ref|NP_000129.2| ─ fibrillin 1 [Homo sapiens]

Length = 2871

Score = 21.8 bits (44), Expect = 1131
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 2 ICTCPK 7
+CTCPK
Sbjct: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 100 CTCP 103

⌈>gi|8217484|emb|CAB92742.1| dJ1092A11.2 (tumor protein p73) [Homo sapiens]
Length = 661

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 319 ICACPGRD 326

⌈>gi|2370178|emb|CAA72221.1| **L** second splice variant [Homo sapiens]
Length = 588

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 246 ICACPGRD 253

⌈>gi|15678984|ref|NP_276101.1| conserved protein [Methanothermobacter thermautotrophicus]
gi|7446472|pir|C69229 conserved hypothetical protein MTH966 - Methanobacterium
thermoautotrophicum (strain Delta H)
gi|2622064|gb|AAB85462.1| conserved protein [Methanothermobacter thermautotrophicus]
Delta H]
Length = 444

Score = 21.8 bits (44), Expect = 1131
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 ICTCPKR 8
ICTC KR
Sbjct: 355 ICTCGKR 361

☐ >gi|21264484|sp|P79820|P53_ORYLA Cellular tumor antigen p53 (Tumor suppressor p53)
gi|4101544|gb|AAD01195.1| tumor suppressor protein p53 [Oryzias latipes]
Length = 352

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 255 ICACPGRD 262

☐ >gi|1184759|gb|AAA87577.1| p53 tumor suppressor homolog
Length = 189

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 90 ICACPGRD 97

☐ >gi|1184757|gb|AAA87576.1| p53 tumor suppressor homolog
Length = 228

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 98 ICACPGRD 105

☐ >gi|7248450|gb|AAF43491.1| p51 isoform delNalpha [Homo sapiens]
Length = 586

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 2 ICTCPKRD 9
IC CP RD
Sbjct: 250 ICACPGRD 257

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Jul 10, 2003 1:49 AM

Number of letters in database: 474,244,320
Number of sequences in database: 1,477,204

Lambda	K	H
0.357	0.293	2.11

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Hits to DB: 7,800,424

Number of Sequences: 1477204

Number of extensions: 35432

Number of successful extensions: 2351

Number of sequences better than 20000.0: 100

Number of HSP's better than 20000.0 without gapping: 2143

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2351

length of query: 9

length of database: 474,244,320

effective HSP length: 0

effective length of query: 9

effective length of database: 474,244,320

effective search space: 4268198880

effective search space used: 4268198880

T: 11

A: 40

X1: 14 (7.2 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 35 (19.8 bits)

S2: 35 (18.0 bits)

Clustal-W Alignment

CLUSTAL W (1.82) multiple sequence alignment

```

gi|21355617|ref|NP_651115.1|  -----MYISQPMSTWHKES-----
gi|25009887|gb|AAN71112.1|  WSTEDSCGHKSQLLNKIYLFECTAMSLHKSASFSLTFNQNTSIVSRNSNR
                               :: . . ** * .:

gi|21355617|ref|NP_651115.1|  -----
gi|25009887|gb|AAN71112.1|  TIFEAFKEFLDFWDIGNEVSAESAVRVSSNGAFNLPQSFGNESNEYAHLA

gi|21355617|ref|NP_651115.1|  -----TDS
gi|25009887|gb|AAN71112.1|  TPVDPAYGGNNTNNMMQFTNNLEILANNNSDGNKINACNKFVCHKGTDS
                               ***

gi|21355617|ref|NP_651115.1|  EDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQSVLR
gi|25009887|gb|AAN71112.1|  EDDSTEVDIKEDIPKTVEVSGSELTTEPMAFLQGLNSGNLMQFSQQSVLR
                               *****

gi|21355617|ref|NP_651115.1|  EMMLQDIQIQANTLPKLENHNIGGYCFSMVLDEPPKSLWMYSIPLNKLYI
gi|25009887|gb|AAN71112.1|  EMMLQDIQIQANTLPKLENHNIGGYCFSMVLDEPPKSLWMYSIPLNKLYI
                               *****

gi|21355617|ref|NP_651115.1|  RMNKAFNVDVQFKSKMPIQPLNLRVFLCFSNDVSAPVVRCQNHLSEPLT
gi|25009887|gb|AAN71112.1|  RMNKAFNVDVQFKSKMPIQPLNLRVFLCFSNDVSAPVVRCQNHLSEPLT
                               *****

gi|21355617|ref|NP_651115.1|  ANNAKMRESLLRSENPNVYCGNAQKGKISERFSVVVPLNMSRSVTRSGL
gi|25009887|gb|AAN71112.1|  ANNAKMRESLLRSENPNVYCGNAQKGKISERFSVVVPLNMSRSVTRSGL
                               *****

gi|21355617|ref|NP_651115.1|  TRQTLAFKFVCQNSCIGRKETSLVFCLEKACGDIVGQHVIVKICTCPKR
gi|25009887|gb|AAN71112.1|  TRQTLAFKFVCQNSCIGRKETSLVFCLEKACGDIVGQHVIVKICTCPKR
                               *****

gi|21355617|ref|NP_651115.1|  DRIQDERQLNSKKRKSVPAAEEDEPSKVRRRCIAIKTEDTESNDSRDCCD
gi|25009887|gb|AAN71112.1|  DRIQDERQLNSKKRKSVPAAEEDEPSKVRRRCIAIKTEDTESNDSRDCCD
                               *****

gi|21355617|ref|NP_651115.1|  SAAEWNVSRTPDGDYRLAITCPNKEWLLQSIEGMIKEAAA EVLRNPNQEN
gi|25009887|gb|AAN71112.1|  SAAEWNVSRTPDGDYRLAITCPNKEWLLQSIEGMIKEAAA EVLRNPNQEN
                               *****

gi|21355617|ref|NP_651115.1|  LRRHANKLLSLKKRAYELP
gi|25009887|gb|AAN71112.1|  LRRHANKLLSLKKRAYELP
                               *****

```

- ☐ Change sequences
- ☐ Align subset of sequences
- ☐ Use Alignment Viewer (new!)
- ☐ Use Tree Viewer (new!)
- ☐ Boxshade ClustalW Alignment (HTML)
- ☐ Boxshade ClustalW Alignment (PostScript)



Nucleotide

Protein

formatting **BLAST**

Translations

Retrieve results for an
RID

Your request has been successfully submitted and put into the Blast Queue.

Query = gi|31207283|ref|XP_312608.1| ENSANGP00000014785 [Anopheles gambiae] (338 letters)

Putative conserved domains have been detected, click on the image below for detailed results.



The request ID is

or

The results are estimated to be ready in 4 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi in

Number of: Descriptions Alignments

Alignment view

Format for PSI-BLAST ☐ with inclusion threshold:

Limit results by or select from:

Expect value range:

EXHIBIT D



results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Ref rence:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1060208428-027529-6850

Query= gi|31207283|ref|XP_312608.1| ENSANGP00000014785
[Anopheles gambiae]
(338 letters)

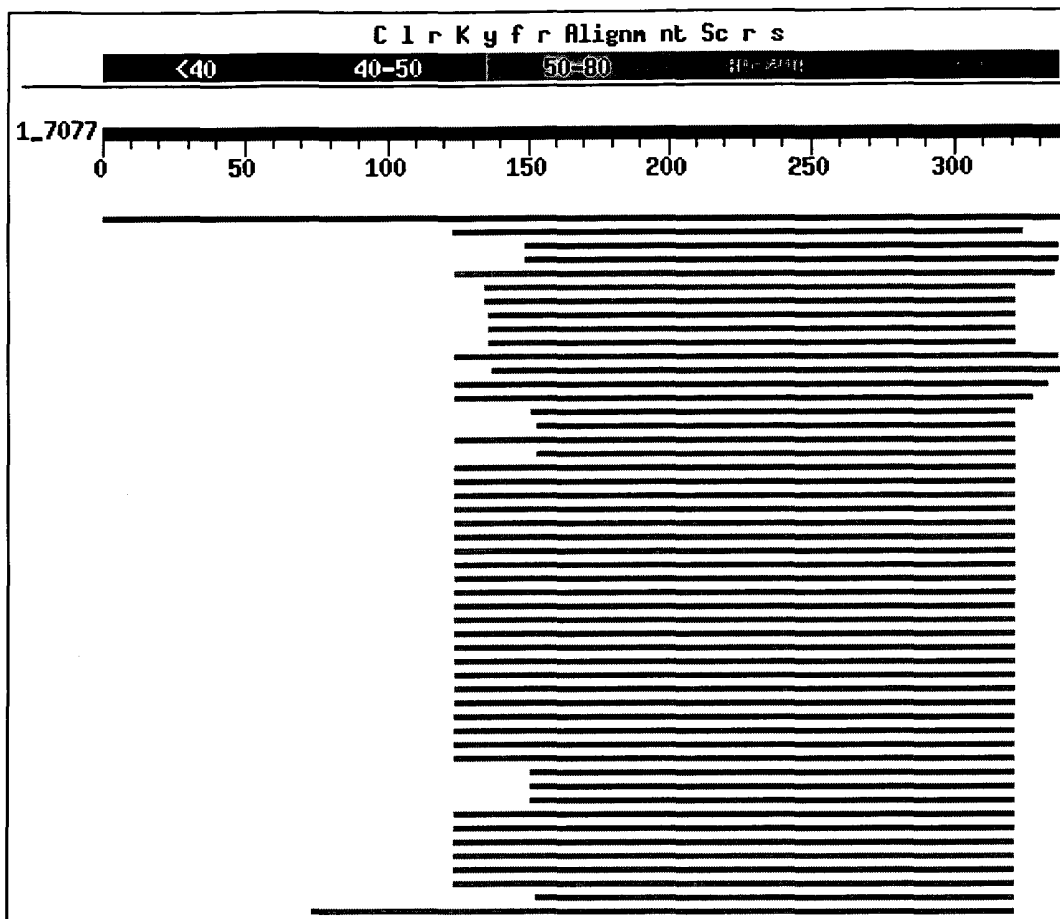
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
1,486,004 sequences; 478,769,834 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Related Structures

Sequences producing significant alignments:			Score (bits)	E Value
gi 31207283 ref XP_312608.1	ENSANGP00000014785	[Anopheles ...	692	0.0
gi 31209247 ref XP_313590.1	ENSANGP00000013376	[Anopheles ...	114	2e-24
gi 21355617 ref NP_651115.1	CG10873-PA	[Drosophila melanog...	97	3e-19
gi 25009887 gb AAN71112.1	AT28346p	[Drosophila melanogaster]	97	3e-19
gi 2811079 sp O12946 P53_PLAFE	Cellular tumor antigen p53 (...		74	5e-12
gi 1244764 gb AAA98564.1	p53 tumor suppressor homolog		73	6e-12
gi 1244762 gb AAA98563.1	p53 tumor suppressor homolog		73	6e-12
gi 19850152 gb AAL99584.1 AF285104_1	p53-like transcription...		69	1e-10
gi 7689271 gb AAF67733.1 AF253323_1	p53 tumor suppressor-li...		69	1e-10
gi 7689273 gb AAF67734.1 AF253324_1	p73-like protein [Mya a...		69	1e-10
gi 10720196 sp Q9W679 P53_TETMU	Cellular tumor antigen p53 ...		67	3e-10
gi 129372 sp P10361 P53_RAT	Cellular tumor antigen p53 (Tum...		67	4e-10
gi 18997097 gb AAL83290.1 AF475081_1	P53 [Delphinapterus le...		66	7e-10
gi 1000577 gb AAB42022.1	p53 [Canis familiaris]		66	7e-10
gi 29470179 gb AAO74632.1	p73 [Danio rerio]		66	7e-10
gi 129368 sp P10360 P53_CHICK	Cellular tumor antigen p53 (T...		66	7e-10
gi 15072750 emb CAC48053.1	p63 delta [Homo sapiens]		66	9e-10
gi 10720186 sp Q9TUB2 P53_PIG	Cellular tumor antigen p53 (T...		66	1e-09
gi 7248450 gb AAF43491.1	p51 isoform delNalpha [Homo sapiens]		65	1e-09
gi 13751173 emb CAC37098.1	TA1 KET alpha protein [Rattus n...		65	1e-09
gi 13751175 emb CAC37099.1	DN KET alpha protein [Rattus no...		65	1e-09

gi 3695094 gb AAC62641.1	TA*p63 alpha [Mus musculus] >gi 3...	65	1e-09	L
gi 9507209 ref NP_062094.1	transformation related protein ...	65	1e-09	L
gi 3510330 dbj BAA32593.1	p51B [Homo sapiens] >gi 7248446 ...	65	1e-09	L
gi 3644040 gb AAC43038.1	CUSP [Homo sapiens] >gi 3695084 g...	65	1e-09	L
gi 31543818 ref NP_003713.3	tumor protein p73-like; tumor ...	65	1e-09	L
gi 13751185 emb CAC37104.1	TA1 KET beta protein [Rattus no...	65	1e-09	L
gi 3695082 gb AAC62635.1	TA p63 alpha [Homo sapiens]	65	1e-09	L
gi 7248451 gb AAF43492.1	p51 isoform delNbeta [Homo sapiens]	65	1e-09	
gi 3970717 emb CAA76562.1	KET protein [Homo sapiens]	65	1e-09	L
gi 6755883 ref NP_035771.1	transformation related protein ...	65	1e-09	L
gi 7248447 gb AAF43488.1	p51 isoform TAp63beta [Homo sapiens]	65	1e-09	
gi 13751187 emb CAC37105.1	DN KET beta protein [Rattus nor...	65	1e-09	L
gi 4996230 dbj BAA78379.1	P53 [Canis familiaris]	65	1e-09	
gi 6093639 sp Q29537 P53_CANFA	Cellular tumor antigen p53 (...)	65	1e-09	
gi 13751183 emb CAC37103.1	TA2 KET beta protein [Rattus no...	65	1e-09	L
gi 12024745 gb AAG45608.1	TA p63 beta [Homo sapiens]	65	1e-09	
gi 3695090 gb AAC62639.1	TA*p63 gamma [Mus musculus] >gi 3...	65	1e-09	L
gi 3695088 gb AAC62638.1	DN p63 beta [Homo sapiens] >gi 12...	65	1e-09	L
gi 13751177 emb CAC37100.1	TA1 KET gamma protein [Rattus n...	65	1e-09	L
gi 3695086 gb AAC62637.1	TA p63 beta [Homo sapiens]	65	1e-09	L
gi 3695092 gb AAC62640.1	TA*p63 beta [Mus musculus] >gi 32...	65	1e-09	L
gi 1463021 gb AAC37335.1	p53 [Canis familiaris]	65	1e-09	
gi 13751181 emb CAC37102.1	DN KET gamma protein [Rattus no...	65	2e-09	L
gi 3695096 gb AAC62642.1	DN p63 gamma [Mus musculus] >gi 3...	65	2e-09	L
gi 3695098 gb AAC62643.1	DN p63 beta [Mus musculus] >gi 32...	65	2e-09	L
gi 13751179 emb CAC37101.1	TA2 KET gamma protein [Rattus n...	65	2e-09	L
gi 12643523 sp Q9XSK8 P73_CERAE	Tumor protein p73 (p53-like...	65	2e-09	
gi 3273745 gb AAC24830.1	p53 homolog [Homo sapiens]	65	2e-09	L
gi 2842672 sp Q64662 P53_SPEBE	Cellular tumor antigen p53 (...)	65	2e-09	
gi 26339452 dbj BAC33397.1	unnamed protein product [Mus mu...	65	2e-09	
gi 3695080 gb AAC62634.1	DN p63 gamma [Homo sapiens] >gi 7...	65	2e-09	L
gi 3510328 dbj BAA32592.1	p51A [Homo sapiens] >gi 3695078 ...	65	2e-09	L
gi 12024746 gb AAG45609.1	TA p63 gamma [Homo sapiens]	65	2e-09	
gi 5353744 gb AAD42225.1	p53 protein [Canis familiaris]	65	2e-09	
gi 7248448 gb AAF43489.1	p51 isoform TAp63delta [Homo sapi...	65	2e-09	
gi 7248452 gb AAF43493.1	p51 isoform delNdelta [Homo sapiens]	65	2e-09	
gi 11342599 emb CAC17147.1	transformation related protein ...	65	2e-09	L
gi 4803651 emb CAA72225.1	P73 splice variant [Cercopithec...	65	2e-09	
gi 23308685 ref NP_689454.1	deltaNp63 isoform alpha 2; tum...	65	2e-09	L
gi 23308709 ref NP_694518.1	deltaNp63 isoform alpha 1; tum...	65	2e-09	L
gi 2833362 sp Q29480 P53_EQUAS	Cellular tumor antigen p53 (...)	64	2e-09	
gi 1938365 gb AAB80959.1	mutant p53 [Rattus norvegicus]	64	3e-09	L
gi 1389675 gb AAB18936.1	tumor-suppressor [Equus caballus]	64	3e-09	
gi 13195250 gb AAK15622.1 AF314148_1	p63 DNA binding protei...	64	3e-09	
gi 19909981 dbj BAB87244.1	deltaN p73 alpha [Homo sapiens]...	64	3e-09	L
gi 20850793 ref XP_131858.1	transformation related protein...	64	3e-09	L
gi 7320915 emb CAB81954.1	P73 delta-N protein [Mus musculus]	64	3e-09	L
gi 12060487 dbj BAB20631.1	DN p63 alpha [Gallus gallus]	64	3e-09	
gi 2370178 emb CAA72221.1	P73 [Homo sapiens]	64	3e-09	L

gi 19909983 dbj BAB87245.1	deltaN p73 beta [Homo sapiens] ...	64	3e-09	L
gi 4885645 ref NP_005418.1	tumor protein p73; p53-related ...	64	3e-09	L
gi 2370177 emb CAA72219.1	P73 [Homo sapiens]	64	3e-09	L
gi 20428532 gb AAK81886.1	DN p73 gamma [Homo sapiens]	64	3e-09	L
gi 10720193 sp Q92143 P53_XIPMA	Cellular tumor antigen p53 ...	64	3e-09	
gi 14719450 pdb 1HU8 A	Chain A, Crystal Structure Of The Mo...	64	4e-09	S
gi 1836145 gb AAB46899.1	sequence-specific transcription f...	64	4e-09	
gi 26348179 dbj BAC37729.1	unnamed protein product [Mus mu...	64	4e-09	L
gi 23308711 ref NP_694519.1	deltaNp63 isoform gamma; tumor...	64	4e-09	L
gi 2829679 sp P79892 P53_HORSE	Cellular tumor antigen p53 (...)	64	5e-09	
gi 10720191 sp O57538 P53_XIPHE	Cellular tumor antigen p53 ...	64	5e-09	
gi 481535 pir S38824	cellular tumor antigen p53, minor spl...	64	5e-09	L
gi 4689086 gb AAD27752.1 AF043641_1	p73 [Barbus barbus]	64	5e-09	
gi 10720192 sp O93379 P53_ICTPU	Cellular tumor antigen p53 ...	64	5e-09	
gi 10720195 sp Q9W678 P53_BARBU	Cellular tumor antigen p53 ...	64	5e-09	
gi 1813455 gb AAB41833.1	p53	64	5e-09	
gi 1813451 gb AAB41831.1	p53	64	5e-09	
gi 28975327 gb AAO60156.1	tumor suppressor p53; p53as [Mus...	63	5e-09	L
gi 13591878 ref NP_112251.1	tumor protein p53; tumor prote...	63	6e-09	L
gi 1813453 gb AAB41832.1	p53	63	6e-09	
gi 53571 emb CAA25323.1	unnamed protein product [Mus muscu...	63	6e-09	L
gi 29468129 gb AAO85406.1 AF365873_1	tumor suppressor p53 [...]	63	6e-09	L
gi 6755881 ref NP_035770.1	transformation related protein ...	63	6e-09	L
gi 129371 sp P02340 P53_MOUSE	Cellular tumor antigen p53 (T...	63	7e-09	L
gi 15375072 gb AAK94783.1	transformation related protein 5...	63	7e-09	L
gi 3445484 dbj BAA32433.1	p73H [Homo sapiens]	63	8e-09	L
gi 1813457 gb AAB41834.1	p53	63	9e-09	
gi 2961247 gb AAC05704.1	tumor suppressor p53 [Mus musculus]	62	1e-08	L
gi 18859503 ref NP_571402.1	tumor protein p53; tumor suppr...	62	1e-08	L
gi 12856636 dbj BAB30732.1	unnamed protein product [Mus mu...	62	1e-08	L

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|31207283|ref|XP_312608.1| ENSANGP00000014785 [Anopheles gambiae]
gi|21295812|gb|EAA07957.1| ENSANGP00000014785 [Anopheles gambiae str. PEST]
Length = 338

Score = 692 bits (1786), Expect = 0.0

Identities = 338/338 (100%), Positives = 338/338 (100%)

Query: 1 MGEKLATSVIECDLCVPRCESDHVVIKSSFIRSYAMASNMEMLNGEIFGDINTALYQNGE 60
MGEKLATSVIECDLCVPRCESDHVVIKSSFIRSYAMASNMEMLNGEIFGDINTALYQNGE
Sbjct: 1 MGEKLATSVIECDLCVPRCESDHVVIKSSFIRSYAMASNMEMLNGEIFGDINTALYQNGE 60

Query: 61 DCQSLFRMNTNDLLPQQGSDLSELMLNDFHNGVAEMQCVKYETDAKLLTMLDGREEPT 120
DCQSLFRMNTNDLLPQQGSDLSELMLNDFHNGVAEMQCVKYETDAKLLTMLDGREEPT
Sbjct: 61 DCQSLFRMNTNDLLPQQGSDLSELMLNDFHNGVAEMQCVKYETDAKLLTMLDGREEPT 120

Query: 121 HYKKIPVLDDFTHPLLQFNVAISGKPCSASAWCYSNALEKLFVKKKTPVTFDVTYMQPSD 180
 HYKKIPVLDDFTHPLLQFNVAISGKPCSASAWCYSNALEKLFVKKKTPVTFDVTYMQPSD
 Sbjct: 121 HYKKIPVLDDFTHPLLQFNVAISGKPCSASAWCYSNALEKLFVKKKTPVTFDVTYMQPSD 180

Query: 181 YSRLKLRIMLVYSNSQYAYQTISRCQDDIAKDGAKEHVVRCCLNPASFTGREKGV 240
 YSRLKLRIMLVYSNSQYAYQTISRCQDDIAKDGAKEHVVRCCLNPASFTGREKGV
 Sbjct: 181 YSRLKLRIMLVYSNSQYAYQTISRCQDDIAKDGAKEHVVRCCLNPASFTGREKGV 240

Query: 241 NFEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSCPTMERRATTLVFTVENEHGTL 300
 NFEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSCPTMERRATTLVFTVENEHGTL
 Sbjct: 241 NFEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSCPTMERRATTLVFTVENEHGTL 300

Query: 301 LGRKSISVKICSCPKRDMEKDDSKATGGRENNKNKRKH 338
 LGRKSISVKICSCPKRDMEKDDSKATGGRENNKNKRKH
 Sbjct: 301 LGRKSISVKICSCPKRDMEKDDSKATGGRENNKNKRKH 338

>gi|31209247|ref|XP_313590.1| ENSANGP00000013376 [Anopheles gambiae]
 gi|21296914|gb|EAA09059.1| ENSANGP00000013376 [Anopheles gambiae str. PEST]
 Length = 332

Score = 114 bits (286), Expect = 2e-24
 Identities = 69/207 (33%), Positives = 112/207 (54%), Gaps = 19/207 (9%)

Query: 124 KIPVLDDFTHPLLQFNVAISGKPCSASAWCYSNALEKLFVKKKTPVTFDV-----TYMQP 178
 K P +D+ + F V S S + +S L+KLF+K + +FD+ T++ P
 Sbjct: 105 KYPSVDELCPADIHFTVIPSST--QSGGFIFSEQLQKLFKLTDSICSFDIACQLPTFLPP 162

Query: 179 SDYSRLKLRIMLVYSNSQYAYQTISRCQDDIAKDGAKEHVVRCCLNPASFTGREK 238
 + + +R+MLV + +++I+RC IA D + K HVRC N + G +
 Sbjct: 163 TGWY---VRVMLVSLAPESQHESITRCHKHIAHDTGPEEIRK-HVVRCKNEQHEYVGADN 218

Query: 239 GVNFEEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSCPTMERRATTLVFTVENEHG 298
 G FEDR AV V L+ ++ V + L+F+CQN+C +++R T LVFT+EN+ G
 Sbjct: 219 GPFFEDRYAVRVPLD-----DEVLCVKIMLQFVCQNTCFRLDQRRGLVFTLENDQG 270

Query: 299 TLLGRKSISVKICSCPKRDMEKDDSKA 325
 + R+ + VKIC +RDM+ + + A
 Sbjct: 271 NIWARRVVPVKICINYYRRDMQNEQNSA 297

>gi|21355617|ref|NP_651115.1| L CG10873-PA [Drosophila melanogaster]
 gi|7211767|gb|AAF40427.1|AF224713_1 L transcription factor p53 [Drosophila melano
 gi|7211769|gb|AAF40428.1|AF224714_1 L transcription factor p53 [Drosophila melano
 gi|7381624|gb|AAF61572.1|AF244918_1 L p53 tumor suppressor-like protein [Drosophi
 gi|8272608|gb|AAF74277.1|AF250918_1 L transcription factor [Drosophila melanogast
 gi|8453176|gb|AAF75270.1|AF263722_1 L transcription factor p53 [Drosophila melano
 gi|10726710|gb|AAF56087.2| L CG10873-PA [Drosophila melanogaster]
 gi|17861528|gb|AAL39241.1| L GH11591p [Drosophila melanogaster]
 gi|18032162|gb|AAL56639.1|AF192555_1 p53-like regulator of apoptosis and cell cyc
 melanogaster]
 Length = 385

Score = 97.4 bits (241), Expect = 3e-19
 Identities = 64/192 (33%), Positives = 102/192 (53%), Gaps = 17/192 (8%)

Query: 150 SAWCYSNALEKLFVKKKTPVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRCQDDI 209
 S W YS L KL+++ DV + L LR+ L +SN A + RCQ+ +
 Sbjct: 103 SLWMYSIPLNKLYIRMNKA FNVDVQFKSKMPIQPLNLRVFLCFSNDVSA--PVVRCQ NHL 160

Query: 210 AKD--GAKDFAHKEHVVRCLNP DASFTGREKGVNFEDRLAVLVDLN--NGGTPQHLEKQQ 265
 + + A + +E ++R NP++ + G +G +R +V+V LN T L +Q
 Sbjct: 161 SVEPLTANNAKMRESLLRSENPN SVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQT 220

Query: 266 TVPVSLEFLCQNSCPTMERRATTLVFTVENEHGTLLGRKSISVKICSCP KRDM EKDDSKA 325
 ++ +F+CQNSC + R+ T+LVF +E G ++G+ I VKIC+CPKRD +D+
 Sbjct: 221 ---LAFKFVCQNSC--IGRKETSLVFCLEKACGDIVGQHVIHV KICTCPKRDRIQDE--- 272

Query: 326 TGGRENNKNKRK 337
 R+ N KRK
 Sbjct: 273 ---RQLNSKKRK 281

☐ >gi|25009887|gb|AAN71112.1| AT28346p [Drosophila melanogaster]
 Length = 519

Score = 97.4 bits (241), Expect = 3e-19
 Identities = 64/192 (33%), Positives = 102/192 (53%), Gaps = 17/192 (8%)

Query: 150 SAWCYSNALEKLFVKKKTPVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRCQDDI 209
 S W YS L KL+++ DV + L LR+ L +SN A + RCQ+ +
 Sbjct: 237 SLWMYSIPLNKLYIRMNKA FNVDVQFKSKMPIQPLNLRVFLCFSNDVSA--PVVRCQ NHL 294

Query: 210 AKD--GAKDFAHKEHVVRCLNP DASFTGREKGVNFEDRLAVLVDLN--NGGTPQHLEKQQ 265
 + + A + +E ++R NP++ + G +G +R +V+V LN T L +Q
 Sbjct: 295 SVEPLTANNAKMRESLLRSENPN SVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTRQT 354

Query: 266 TVPVSLEFLCQNSCPTMERRATTLVFTVENEHGTLLGRKSISVKICSCP KRDM EKDDSKA 325
 ++ +F+CQNSC + R+ T+LVF +E G ++G+ I VKIC+CPKRD +D+
 Sbjct: 355 ---LAFKFVCQNSC--IGRKETSLVFCLEKACGDIVGQHVIHV KICTCPKRDRIQDE--- 406

Query: 326 TGGRENNKNKRK 337
 R+ N KRK
 Sbjct: 407 ---RQLNSKKRK 415

☐ >gi|2811079|sp|O12946|P53_PLAFE Cellular tumor antigen p53 (Tumor suppressor p53)
 gi|1922902|emb|CAA70123.1| p53 [Platichthys flesus]
 Length = 366

Score = 73.6 bits (179), Expect = 5e-12
 Identities = 58/220 (26%), Positives = 100/220 (45%), Gaps = 23/220 (10%)

Query: 125 IPVLD DDFTHPL-LQFNVAISGKPCSASAWCYSNALEKLFVK--K KTPVTFDVTYMQPSDY 181
 +PV+ D+ Q SG S ++ +S L+KL+ + K +PV ++ P
 Sbjct: 75 VPVVTDPYGEYGFQLRFQKSGTAKSVTS-TFSELLKKLYCQLAKTSPVEVLLSKEPPQGA 133

Query: 182 SRLKLRIMLVYSNSQYAYQTISRCQDDIAKDGA KDFAHKEHVVRCLNP DASFTGREKGVN 241
 LR VY +++ + RC +D A+ H+ H++R G ++ +
 Sbjct: 134 V---LRATAVYKKTEHVADVVRRC PHHQTEDTAE---HRSHLIR-----LEGSQRALY 180

Query: 242 FEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGT L 300

FED + P L +T + L F+C +SC M RR + T+E G +
 Sbjct: 181 FEDPHTKRQSVTPYEPQL-GSETTAILLSFMCNSSCMGMNRRQILTILTLETPDGLV 239

Query: 301 LGRKSISVVKICSCPKRDMEKDDSKAT----GGRENNKNKR 336
 LGR+ V++C+CP RD + D+ +T G ++ K K+
 Sbjct: 240 LGRRCFEVRVCACPGDRKTDEESSTKTPNGPKQTKKRKQ 279

☐ >gi|1244764|gb|AAA98564.1| p53 tumor suppressor homolog
 Length = 391

Score = 73.2 bits (178), Expect = 6e-12
 Identities = 54/194 (27%), Positives = 95/194 (48%), Gaps = 21/194 (10%)

Query: 135 LLQFNVAISGKPCSASAWCYSNALEKLFVKKKT--PVTFDVTYMQPSDYSRLKLRIMLVY 192
 + + + A K ++ W YS L+KL+V+ T PV F PS ++R M +Y
 Sbjct: 133 VFEMSFAQPSKETKSTTWYSEKLDKLYVRMATTCPVRFKTARPPPSG---CQIRAMPIY 189

Query: 193 SNSQYAYQTISRCQDD-IAKDGAKEHVRCLNPASFTGREKGVNFEDRLAVLVD 251
 ++ + + RC + AK+ + H+VRC + A + + + R +VL+
 Sbjct: 190 MKPEHVQEVVKRCPNHATAKEHNEKHPAPLHIVRCEHKLAKYHEDK----YSGRQSVLI- 244

Query: 252 LNNGGTPQHLEK--QQTPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISV 308
 P + + + V +F+C SC RR LVFT+E ++ +LGR+++ V
 Sbjct: 245 -----PHEMPQAGSEWVNLYQFMCLGSCVGGPNRRPIQLVFTLEKDN-QVLGRRAVEV 297

Query: 309 KICSCPKRDMEKDD 322
 +IC+CP RD + D+
 Sbjct: 298 RICACPGDRKKADE 311

☐ >gi|1244762|gb|AAA98563.1| p53 tumor suppressor homolog
 Length = 564

Score = 73.2 bits (178), Expect = 6e-12
 Identities = 54/194 (27%), Positives = 95/194 (48%), Gaps = 21/194 (10%)

Query: 135 LLQFNVAISGKPCSASAWCYSNALEKLFVKKKT--PVTFDVTYMQPSDYSRLKLRIMLVY 192
 + + + A K ++ W YS L+KL+V+ T PV F PS ++R M +Y
 Sbjct: 133 VFEMSFAQPSKETKSTTWYSEKLDKLYVRMATTCPVRFKTARPPPSG---CQIRAMPIY 189

Query: 193 SNSQYAYQTISRCQDD-IAKDGAKEHVRCLNPASFTGREKGVNFEDRLAVLVD 251
 ++ + + RC + AK+ + H+VRC + A + + + R +VL+
 Sbjct: 190 MKPEHVQEVVKRCPNHATAKEHNEKHPAPLHIVRCEHKLAKYHEDK----YSGRQSVLI- 244

Query: 252 LNNGGTPQHLEK--QQTPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISV 308
 P + + + V +F+C SC RR LVFT+E ++ +LGR+++ V
 Sbjct: 245 -----PHEMPQAGSEWVNLYQFMCLGSCVGGPNRRPIQLVFTLEKDN-QVLGRRAVEV 297

Query: 309 KICSCPKRDMEKDD 322
 +IC+CP RD + D+
 Sbjct: 298 RICACPGDRKKADE 311

☐ >gi|19850152|gb|AAL99584.1|AF285104_1 p53-like transcription factor p120 [Spisu]
 Length = 591

Score = 68.9 bits (167), Expect = 1e-10

Identities = 51/190 (26%), Positives = 93/190 (48%), Gaps = 17/190 (8%)

Query: 137 QFNVAISGKPCSASAWCYSNALEKLFVKKKT--PVTFDVTYMQPSDYSRLKLRIMLVYSN 194
 ++ A K ++ W YS+ L+KL+V+ T PV F P+ +R M ++

Sbjct: 143 EISFATPSKETKSTTWTYSDMLKKLYVRMATTCPVRFKTNRQPPAG---CIIRSMPIFMK 199

Query: 195 SQYAYQTISRCQDD-IAKDGAkdFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLN 253
 ++ ++ RC + +K+ ++ H+VRC + A + + R +V++

Sbjct: 200 PEHVQEAVKRCPNHATSKEFNENHPAPNHLVRCHEKLAkyVEDP----YTSRQSVVIPQE 255


Query: 254 NGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICS 312
 TPQ + V +F+C SC RR +VFT+E ++ +LGR+ + V+IC+

Sbjct: 256 ---TPQ--AGSEWVTNLFQFMCLGSCVGGPNRRPLQIVFTLEKDN-QVLGRRCVEVRICA 309

Query: 313 CPKRDMEKDD 322

CP RD + D+

Sbjct: 310 CPGRDRKGDE 319

 >gi|7689271|gb|AAF67733.1|AF253323_1 p53 tumor suppressor-like protein [Mya arer
 Length = 443

Score = 68.9 bits (167), Expect = 1e-10

Identities = 51/190 (26%), Positives = 93/190 (48%), Gaps = 17/190 (8%)

Query: 137 QFNVAISGKPCSASAWCYSNALEKLFVKKKT--PVTFDVTYMQPSDYSRLKLRIMLVYSN 194
 ++ A K ++ W YS+ L+KL+V+ T PV F P +R M ++

Sbjct: 149 EISFATPSKETKSTTWTYSDILKKLYVRMATTCPVRFKTLRQPPPG---CVIRSMPIFMK 205

Query: 195 SQYAYQTISRCQDD-IAKDGAkdFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLN 253
 ++ ++ RC + +K+ ++ H+VRC + + + +R +VL+

Sbjct: 206 PEHVQEAVKRCPNHATSKEFNENHPAPNHLVRCHEKVKskyVEDP----YTNRQSVLIPQE 261


Query: 254 NGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICS 312
 TPQ + V +F+C SC RR +VFT+E ++ +LGR+ + V+IC+

Sbjct: 262 ---TPQ--AGSEWVTNLFQFMCLGSCVGGPNRRPLQIVFTLEKDN-QVLGRRCVEVRICA 315

Query: 313 CPKRDMEKDD 322

CP RD + D+

Sbjct: 316 CPGRDRKADE 325

 >gi|7689273|gb|AAF67734.1|AF253324_1 p73-like protein [Mya arenaria]
 Length = 621

Score = 68.6 bits (166), Expect = 1e-10

Identities = 51/190 (26%), Positives = 93/190 (48%), Gaps = 17/190 (8%)

Query: 137 QFNVAISGKPCSASAWCYSNALEKLFVKKKT--PVTFDVTYMQPSDYSRLKLRIMLVYSN 194
 ++ A K ++ W YS+ L+KL+V+ T PV F P +R M ++


Sbjct: 149 EISFATPSKETKSTTWTYSDILKKLYVRMATTCPVRFKTLRQPPPG---CVIRSMPIFMK 205

Query: 195 SQYAYQTISRCQDD-IAKDGAkdFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLN 253
 ++ ++ RC + +K+ ++ H+VRC + + + +R +VL+

Sbjct: 206 PEHVQEAVKRCPNHATSKEFNENHPAPNHLVRCHEKVKskyVEDP----YTNRQSVLIPQE 261

Query: 254 NGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICS 312
 TPQ + V +F+C SC RR +VFT+E ++ +LGR+ + V+IC+
 Sbjct: 262 ---TPQ--AGSEWVTNLFQFMCLGSCVGGPNRRPLQIVFTLEKDN-QVLGRRCVEVRICA 315

Query: 313 CPKRDMEKDD 322
 CP RD + D+
 Sbjct: 316 CPGRDRKADE 325

 >gi|10720196|sp|Q9W679|P53_TETMU Cellular tumor antigen p53 (Tumor suppressor p53)
 gi|4959052|gb|AAD34213.1|AF071571.1 tumor suppressor protein p53 [Tetraodon miurus]
 Length = 367



Score = 67.4 bits (163), Expect = 3e-10
 Identities = 52/217 (23%), Positives = 99/217 (45%), Gaps = 19/217 (8%)

Query: 125 IPVLDDFTHPL---LQFNVAISGKPCASAWCYSNALEKLFVKKKTPVTFDVTYMQPSDY 181
 +PV D+ L+F + + K +++ YS L KL+ + +V +
 Sbjct: 81 VPVTTDYPGEYGFKLRFQKSGTAKSVTST---YSEILNKLYCQLAKTSLVEVLLGKDPPM 137

Query: 182 SRLKLRIMLVYSNSQYAYQTISRCQDDIAKDGAKEHVVRCLNPASFTGREKGVN 241
 + LR +Y +++ + + RC +D A+ H+ H++R G E+
 Sbjct: 138 GAV-LRATAIYKKTEHVAEVVRRCPHHQNEDESAE---HRSHLIR-----MEGSERAQY 186

Query: 242 FEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLL 300
 FE + P L + T + L F+C +SC M RR + T+E + G +
 Sbjct: 187 FEHPHTKRQSVTVPYEPPQLGSEFTT-ILLSFMCNSSCMGGMNRRPILITILTLETQEGIV 245

Query: 301 LGRKSISVKICSCPKRDMEKDDSKATGGRENNKKNKRK 337
 LGR+ V++C+CP RD + +++ +T + + K+ +K
 Sbjct: 246 LGRRCFEVRVCACPRDRKTEETNSTKMQNDADAKK 282

 >gi|129372|sp|P10361|P53_RAT Cellular tumor antigen p53 (Tumor suppressor p53)
 gi|92070|pir|S02192 cellular tumor antigen p53 - rat
 gi|56829|emb|CAA31457.1|  unnamed protein product [Rattus norvegicus]
 Length = 391

Score = 67.0 bits (162), Expect = 4e-10
 Identities = 56/206 (27%), Positives = 89/206 (43%), Gaps = 24/206 (11%)

Query: 138 FNVAISGKPCASAWC-YNALEKLFVK--KKTPTVTFDVTYMQPSDYSRLKLRIMLVYSN 194
 F++ + S C YS +L KLF + K PV VT P ++R M +Y
 Sbjct: 107 FHLGFLQSGTAKSVMCTYSISLNKLFQQLAKTCPVQLWVTSTPPPG---TRVRAMAIYKK 163

Query: 195 SQYAYQTISRCQDDIAKDGAKEHVVRCL-NPDASFTGREKGVNFEDRLAVLVDLN 253
 SQ+ + + RC A +H++R NP A + +DR +
 Sbjct: 164 SQHMTVEVRRCPHHERCSDGDGLAPPQHILIRVEGNPYAEY-----LDDRQTFRHSVV 215

Query: 254 NGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICS 312
 P + T + ++C +SC M RR + T+E+ G LLGR S V++C+
 Sbjct: 216 VPYEPPEVGSDYTT-IHYKMCNSSCMGGMNRRPILITIITLEDSSGNLLGRDSFEVRVCA 274

Query: 313 CPKRDMEKDDSKATGGRENNKKNKRKH 338
 CP RD ++ EN + K +H
 Sbjct: 275 CPGRDRRTEE-----ENFRKKEEH 293

☐ >gi|18997097|gb|AAL83290.1|AF475081_1 P53 [Delphinapterus leucas]
Length = 387

Score = 66.2 bits (160), Expect = 7e-10
Identities = 49/173 (28%), Positives = 78/173 (45%), Gaps = 15/173 (8%)

Query: 154 YSNALEKLFVK--KKTPTVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRC-QDDIA 210
YS AL KLF + K PV V+ P ++R M +Y S+Y + + RC +
Sbjct: 119 YSPALNKLFCQLAKTCPVQLWVSSPPPPG---TRVRAMAIYKKSEYMTEVVRRCPPHERC 175

Query: 211 KDGAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVPVS 270
D + A +H++R G + +DR + P + T +
Sbjct: 176 SDYS DGLAPPQH LIRV-----EGNLR AEYLDD RNTFRHSV VVPYEPPEVGS DCTT-IH 227

Query: 271 LEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICSCPKRDM EKDD 322
F+C +SC M RR + T+E+ +G LLGR S V++C+CP RD ++
Sbjct: 228 YNFM CNSSCMGGMNRRPILTIITLED SNGNLLGRNSFEVRVCACPGDRDRTEE 280

☐ >gi|1000577|gb|AAB42022.1| p53 [Canis familiaris]
Length = 276

Score = 66.2 bits (160), Expect = 7e-10
Identities = 46/175 (26%), Positives = 77/175 (44%), Gaps = 15/175 (8%)

Query: 152 WCYSNALEKLFVK--KKTPTVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRC-QDD 208
W YS L KLF + K PV V+ P + +R M +Y S++ + + RC +
Sbjct: 87 WTYSPLLNKLFCQLAKTCPVQLWVSSPPPPNTC---VRAMAIYKKSEFVTEVVRRCPPHE 143

Query: 209 IAKDGAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVP 268
D + A +H++R G + +DR + P + T
Sbjct: 144 RCS DSS DGLAPPQH LIRV-----EGNLR AKYLDD RNTFRHSV VVPYEPPEVGS DYT T- 195

Query: 269 VSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICSCPKRDM EKDD 322
+ ++C +SC M RR + T+E+ G +LGR S V++C+CP RD ++
Sbjct: 196 IHYNYM CNSSCMGGMNRRPILTIITLED SGNVLGRNSFEVRVCACPGDRDRTEE 250

☐ >gi|29470179|gb|AAO74632.1| p73 [Danio rerio]
Length = 640

Score = 66.2 bits (160), Expect = 7e-10
Identities = 63/233 (27%), Positives = 101/233 (43%), Gaps = 41/233 (17%)

Query: 125 IPVLD DDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLF--VKKKTPVTFDVTYMQPSDY 181
IP D+ P F V + SA W YS L+KL+ + K P+ + P+
Sbjct: 122 IPSNTDYPGP-HNFEVTFQSS TAKSATWTYSPL LKKLYCQIAKTCPIQIKLASSPPNGS 180

Query: 182 SRLKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVR-----CLNPDASF 233
+R M +Y +++ + + RC + + +D A H++R C D
Sbjct: 181 V---IRAMPIYKKAHVTEVVKRCPNHKLGRDFNESQTAPASHLIRVEGNNLCQYVDDPV 237

Query: 234 TGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFT 292
TGR+ +VLV +PQ + T+ + F+C +SC M RR ++ T

Sbjct: 238 TGRQ-----SVLVPYE---SPQVGTEFTTILYN--FMCNSSCVGGMNRRPILIIIT 283

Query: 293 VENEHGTLLGRKSIIVKICSCPKRDMKD-----DSKATGGRENNKN 334

+E G +LGR+S +IC+CP RD + D +S A G N +N

Sbjct: 284 LETRDGQVLGRRSFEGRICACPGDRKADHDHFREQQALNESVAKNGNANKRN 336

☐ >gi|129368|sp|P10360|P53_CHICK Cellular tumor antigen p53 (Tumor suppressor p53)
gi|86220|pir|S02193 cellular tumor antigen p53 - chicken
gi|63741|emb|CAA31456.1| nuclear protein p53 (AA 1 - 367) [Gallus gallus]
Length = 367

Score = 66.2 bits (160), Expect = 7e-10

Identities = 61/212 (28%), Positives = 93/212 (43%), Gaps = 21/212 (9%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASAWC-YSNALEKLFVK--KKTPTVTFDVTYMQPSDY 181
+P +D+ F V + S C YS L K++ + K PV V P

Sbjct: 82 VPSTEDYGGD-FDFRVGFVEAGTAKSVTCTYSPVLNKVYCRLAKPCPVQVRVGVAPPPGS 140

Query: 182 SRLKLRIMLVYSNSQYAYQTISRCQDDIAKDGAKE-FAHKEHVVRCL-NPDASFTGREKG 239
S LR + VY S++ + + RC G D A +H++R NP A + E

Sbjct: 141 S---LRAVAVYKKSEHVAEVVRRCPHHERCGGGTDGLAPAQHILIRVEGNPQARYHDDT- 196

Query: 240 VNFEDRLAVLVDLNNGGTTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENEHG 298
R +V+V P + T V F+C +SC M RR + T+E G

Sbjct: 197 ---TKRHSVVVPYE----PPEVGSDDCTT-VLYNFMCNSSCMGMNRRPILITLTLEGPGG 248

Query: 299 TLLGRKSIIVKICSCPKRD--MEKDDSKATGG 328

LLGR+ V++C+CP RD +E+++ + GG

Sbjct: 249 QLLGRRCFEVRVCACPGDRKIEEENFRKRGG 280

☐ >gi|15072750|emb|CAC48053.1| p63 delta [Homo sapiens]
Length = 232

Score = 65.9 bits (159), Expect = 9e-10

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 13 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 71

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 72 V-IRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRV-----EGNSHAQY 123

Query: 242 FED----RLAVLVDLNNGGTTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 124 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 178

Query: 297 HGTLLGRKSIIVKICSCPKRDMKDD 322

G +LGR+ +IC+CP RD + D+

Sbjct: 179 DGQVLGRRCFEARICACPGDRKADE 204

☐ >gi|10720186|sp|Q9TUB2|P53_PIG Cellular tumor antigen p53 (Tumor suppressor p53)

gi|6165623|gb|AAF04620.1|AF098067_1 tumor suppressor p53 [Sus scrofa]
Length = 386

Score = 65.9 bits (159), Expect = 1e-09
Identities = 49/173 (28%), Positives = 78/173 (45%), Gaps = 15/173 (8%)

Query: 154 YSNALEKLFVK--KKTPTFTDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRC-QDDIA 210
YS AL KLF + K PV V+ P ++R M +Y S+Y + + RC + +
Sbjct: 118 YSPALNKLFCQLAKTCPVQLWVSSPPPPG---TRVRAMAIYKKSEYMTEVVRRCPHHERS 174

Query: 211 KDGAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVPVS 270
D + A +H++R G + +DR + P + T +
Sbjct: 175 SDYS DGLAPPQH LIRV-----EGNLRAEYLDDRNTFRHSVVVPYEPPEVGS DCTT-IH 226

Query: 271 LEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICSCP KRDM EKDD 322
F+C +SC M RR + T+E+ G LLGR S V++C+CP RD ++
Sbjct: 227 YNFM CNSSCMGGMNRRPILTIITLEDASGNLLGRNSFEVRVCACPGRDRRTEE 279

gi|7248450|gb|AAF43491.1| p51 isoform delNalpha [Homo sapiens]
Length = 586

Score = 65.5 bits (158), Expect = 1e-09
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLD DFT HPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + M P
Sbjct: 71 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMT PPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
+ +R M VY +++ + + RC + +++++ A H++R G
Sbjct: 130 V-IRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
ED R +VLV P + + T V F+C +SC M RR ++ T+E
Sbjct: 182 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFM CNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSISVKICSCP KRDM EKDD 322
G +LGR+ +IC+CP RD + D+
Sbjct: 237 DGQVLGRRCFEARICACPGRDRKADE 262

gi|13751173|emb|CAC37098.1| **L** TA1 KET alpha protein [Rattus norvegicus]
Length = 663

Score = 65.5 bits (158), Expect = 1e-09
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLD DFT HPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + M P
Sbjct: 148 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMT PPPQGA 206

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
+ +R M VY +++ + + RC + +++++ A H++R G
Sbjct: 207 V-IRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 258

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296

ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 259 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 313

Query: 297 HGTLLGRKSI SVKICSCP KRDMEKDD 322
 G +LGR+ +IC+CP RD + D+

Sbjct: 314 DGQVLGRRCFEARICACPGDRKDE 339

☐ >gi|13751175|emb|CAC37099.1| ☒ DN KET alpha protein [Rattus norvegicus]
 Length = 586

Score = 65.5 bits (158), Expect = 1e-09
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 71 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 130 V-IRAMPVYKKAHVTEVVKRCPNHEL SREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVLDLNNGGTPOHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 182 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSI SVKICSCP KRDMEKDD 322
 G +LGR+ +IC+CP RD + D+

Sbjct: 237 DGQVLGRRCFEARICACPGDRKDE 262

☐ >gi|3695094|gb|AAC62641.1| ☒ TA*p63 alpha [Mus musculus]
 gi|32812141|gb|AAP87982.1| p63 TA alpha [Mus musculus]
 Length = 680

Score = 65.5 bits (158), Expect = 1e-09
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 165 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 224 V-IRAMPVYKKAHVTEVVKRCPNHEL SREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVLDLNNGGTPOHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 276 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLLGRKSI SVKICSCP KRDMEKDD 322
 G +LGR+ +IC+CP RD + D+

Sbjct: 331 DGQVLGRRCFEARICACPGDRKDE 356

☐ >gi|9507209|ref|NP_062094.1| ☒ transformation related protein 63; tumor protein

norvegicus]

gi|7630117|emb|CAB88216.1| **L** TA2 KET alpha [Rattus norvegicus]
Length = 680

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 165 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDSFTGREKGVN 241
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 224 V-IRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 276 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLLGRKSI SVKICSCP KRDMEKDD 322

G +LGR+ +IC+CP RD + D+

Sbjct: 331 DGQVLGRRCFEARICACPGDRKDE 356

L >gi|3510330|dbj|BAA32593.1| **L** p51B [Homo sapiens]
gi|7248446|gb|AAF43487.1| p51 isoform TAp63alpha [Homo sapiens]
Length = 641

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + + M P

Sbjct: 126 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 184

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDSFTGREKGVN 241
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 185 V-IRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 236

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 237 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 291

Query: 297 HGTLLGRKSI SVKICSCP KRDMEKDD 322

G +LGR+ +IC+CP RD + D+

Sbjct: 292 DGQVLGRRCFEARICACPGDRKDE 317

L >gi|3644040|gb|AAC43038.1| **L** CUSP [Homo sapiens]
gi|3695084|gb|AAC62636.1| **L** DN p63 alpha [Homo sapiens]
gi|12024747|gb|AAG45610.1| DN p63 alpha [Homo sapiens]
Length = 586

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183

IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 130 V-IRAMPVYKKAHVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVLDLNNGGTPOHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 182 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCSNCSVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSIISVKICSCPKRDMKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 237 DGQVLGRRCFEARICACPGDRDKADE 262

☐ >gi|31543818|ref|NP_003713.3| ☒ tumor protein p73-like; tumor protein 63 kDa wit
 to p53; tumor protein p63 [Homo sapiens]
 gi|12024744|gb|AAG45607.1| TA p63 alpha [Homo sapiens]
 gi|24980977|gb|AAH39815.1| ☒ tumor protein p63 [Homo sapiens]
 Length = 680

Score = 65.5 bits (158), Expect = 1e-09
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 165 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 224 V-IRAMPVYKKAHVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVLDLNNGGTPOHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 276 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCSNCSVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLLGRKSIISVKICSCPKRDMKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 331 DGQVLGRRCFEARICACPGDRDKADE 356

☐ >gi|13751185|emb|CAC37104.1| ☒ TA1 KET beta protein [Rattus norvegicus]
 Length = 538

Score = 65.5 bits (158), Expect = 1e-09
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 148 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 206

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 207 V-IRAMPVYKKAHVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 258

Query: 242 FED----RLAVLVLDLNNGGTPOHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296

ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 259 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 313

Query: 297 HGTLLGRKSI SVKICSCP KRDMEKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 314 DGQVLGRRCFEARICACPGDRK ADE 339

☐ >gi|3695082|gb|AAC62635.1| ☒ TA p63 alpha [Homo sapiens]
 Length = 641

Score = 65.5 bits (158), Expect = 1e-09
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 126 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 184

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 185 V-IRAMPVYKKAHVTEVVKRCPNHEL SREFNEGQIAPPSHLIRV-----EGNSHAQY 236

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 237 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 291

Query: 297 HGTLLGRKSI SVKICSCP KRDMEKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 292 DGQVLGRRCFEARICACPGDRK ADE 317

☐ >gi|7248451|gb|AAF43492.1| p51 isoform delNbeta [Homo sapiens]
 Length = 461

Score = 65.5 bits (158), Expect = 1e-09
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 130 V-IRAMPVYKKAHVTEVVKRCPNHEL SREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 182 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSI SVKICSCP KRDMEKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 237 DGQVLGRRCFEARICACPGDRK ADE 262

☐ >gi|3970717|emb|CAA76562.1| ☒ KET protein [Homo sapiens]
 Length = 680

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + M P

Sbjct: 165 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPASFTGREKGVN 241
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 224 V-IRAMPVYKKAHVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 276 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLLGRKSISVKICSCPGRDMEKDD 322

G +LGR+ +IC+CP RD + D+

Sbjct: 331 DGQVLGRRCFEARICACPGDRKADE 356

☐ >gi|6755883|ref|NP_035771.1| ☒ transformation related protein 63; KET protein; t
[Mus musculus]

gi|3445482|dbj|BAA32432.1| ☒ p73H [Mus musculus]

gi|3695100|gb|AAC62644.1| ☒ DN p63 alpha [Mus musculus]

gi|32812144|gb|AAP87985.1| p63 DN alpha [Mus musculus]

Length = 586

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + M P

Sbjct: 71 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPASFTGREKGVN 241
+ +R M VY +++ + + RC + +++++ A H++R G

Sbjct: 130 V-IRAMPVYKKAHVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
ED R +VLV P + + T V F+C +SC M RR ++ T+E

Sbjct: 182 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSISVKICSCPGRDMEKDD 322

G +LGR+ +IC+CP RD + D+

Sbjct: 237 DGQVLGRRCFEARICACPGDRKADE 262

☐ >gi|7248447|gb|AAF43488.1| p51 isoform TAp63beta [Homo sapiens]
Length = 516

Score = 65.5 bits (158), Expect = 1e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)



Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + M P

Sbjct: 126 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 184

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 185 V-IRAMPVYKKAHEVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 236

Query: 242 FED----RLAVLVDLNNGGTTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 237 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 291

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 292 DGQVLGRRCFEARICACPGDRKDE 317

 >gi|13751187|emb|CAC37105.1|  DN KET beta protein [Rattus norvegicus]
 Length = 461


Score = 65.5 bits (158), Expect = 1e-09
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 130 V-IRAMPVYKKAHEVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVDLNNGGTTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 182 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 237 DGQVLGRRCFEARICACPGDRKDE 262

 >gi|4996230|dbj|BAA78379.1| P53 [Canis familiaris]
 Length = 381

Score = 65.5 bits (158), Expect = 1e-09
 Identities = 46/175 (26%), Positives = 77/175 (44%), Gaps = 15/175 (8%)

Query: 152 WCYSNALEKLFVK--KKTPTVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRC-QDD 208
 W YS L KLF + K PV V+ P + +R M +Y S++ + + RC +
 Sbjct: 111 WTYSPLLNLKFCQLAKTCPVQLWVSSPPPPNTC---VRAMAIYKKSEFVTEVVRRCPHHE 167

Query: 209 IAKDGAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLNNGGTTPQHLEKQQTVP 268
 D + A +H++R G + +DR + P + T
 Sbjct: 168 RCSDDSDGLAPPQHLIRV-----EGNLRKAYLDDRNTFRHSVVVPYEPPEVGSDDYTT- 219

Query: 269 VSLEFLCQNSC-PTMERRATTLVFTVENEHGTLGRKKSISVKICSCPGRDMEKDD 322
 + ++C +SC M RR + T+E+ G +LGR S V++C+CP RD ++
 Sbjct: 220 IHYNYMCNSSCMGGMNRRPILTIITLEDSSGNVLGRNSFEVRVCACPGDRRTEE 274

☐ >gi|6093639|sp|Q29537|P53_CANFA Cellular tumor antigen p53 (Tumor suppressor p53 protein [Canis familiaris])
gi|3150077|gb|AAC16909.1| p53 protein [Canis familiaris]
Length = 381

Score = 65.5 bits (158), Expect = 1e-09
Identities = 46/175 (26%), Positives = 77/175 (44%), Gaps = 15/175 (8%)

Query: 152 WCYSNALEKLFVK--KKTPVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRC-QDD 208
W YS L KLF + K PV V+ P + +R M +Y S++ + + RC +
Sbjct: 111 WTYSPLLNKLFQCLAKTCPVQLWVSSPPPPNTC---VRAMAIYKKSEFVTEVVRRCPHHE 167

Query: 209 IAKDGAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTVP 268
D + A +H++R G + +DR + P + T
Sbjct: 168 RCSDDSDGLAPPQHILRV-----EGNLRAYLDDRNTFRHSVVVPYEPPEVGSDYTT- 219

Query: 269 VSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICSCPGRDMEKDD 322
+ ++C +SC M RR + T+E+ G +LGR S V++C+CP RD ++
Sbjct: 220 IHNYMCNSSCMGGMNRRPILTIITLEDSSGNVLGRNSFEVRVCACPRDRRTEE 274

☐ >gi|13751183|emb|CAC37103.1| ☒ TA2 KET beta protein [Rattus norvegicus]
Length = 555

Score = 65.5 bits (158), Expect = 1e-09
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + + M P
Sbjct: 165 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
+ +R M VY +++ + + RC + +++++ A H++R G
Sbjct: 224 V-IRAMPVYKKAHVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
ED R +VLV P + + T V F+C +SC M RR ++ T+E
Sbjct: 276 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIVTLETR 330

Query: 297 HGTLGRKSISVKICSCPGRDMEKDD 322
G +LGR+ +IC+CP RD + D+
Sbjct: 331 DGQVLGRRCFEARICACPRDRKADE 356

☐ >gi|12024745|gb|AAG45608.1| TA p63 beta [Homo sapiens]
Length = 555

Score = 65.5 bits (158), Expect = 1e-09
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + + M P
Sbjct: 165 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
+ +R M VY +++ + + RC + +++++ A H++R G
Sbjct: 224 V-IRAMPVYKKAHVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 276 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFCNNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLLGRKSI SVKICSCPKRDM EKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 331 DGQVLGRRCFEARICACPGRDRKADE 356

☐ >gi|3695090|gb|AAC62639.1| ☒ TA*p63 gamma [Mus musculus]
 gi|32812143|gb|AAP87984.1| p63 TA gamma [Mus musculus]
 Length = 483

Score = 65.5 bits (158), Expect = 1e-09
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLD DFT HPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 165 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNP DASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 224 V-IRAMPVYKKA EHVTEVVKRCPNHEL SREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 276 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFCNNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLLGRKSI SVKICSCPKRDM EKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 331 DGQVLGRRCFEARICACPGRDRKADE 356

☐ >gi|3695088|gb|AAC62638.1| ☒ DN p63 beta [Homo sapiens]
 gi|12024748|gb|AAG45611.1| DN p63 beta [Homo sapiens]
 Length = 461

Score = 65.5 bits (158), Expect = 1e-09
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLD DFT HPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNP DASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 130 V-IRAMPVYKKA EHVTEVVKRCPNHEL SREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 182 VEDPITGRQSVLVPYE----PPQVGTEFTT-VLYNFCNNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSI SVKICSCPKRDM EKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 237 DGQVLGRRCFEARICACPGRDRKADE 262

☐ >gi|13751177|emb|CAC37100.1| ☒ TA1 KET gamma protein [Rattus norvegicus]
Length = 470

Score = 65.5 bits (158), Expect = 1e-09
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + + M P
Sbjct: 148 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 206

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
+ +R M VY +++ + + RC + +++++ A H++R G
Sbjct: 207 V-IRAMPVYKKAHVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 258

Query: 242 FED---RLAVLVDLNNGGTTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
ED R +VLV P + + T V F+C +SC M RR ++ T+E
Sbjct: 259 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 313

Query: 297 HGTLLGRKSISVKICSCPKRDMKDD 322
G +LGR+ +IC+CP RD + D+
Sbjct: 314 DGQVLGRRCFEARICACPGRDRKADE 339

☐ >gi|3695086|gb|AAC62637.1| ☒ TA p63 beta [Homo sapiens]
Length = 516

Score = 65.5 bits (158), Expect = 1e-09
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + + M P
Sbjct: 126 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 184

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
+ +R M VY +++ + + RC + +++++ A H++R G
Sbjct: 185 V-IRAMPVYKKAHVTEVVKRCPNHELSREFNEGQIAPPSHLIRV-----EGNSHAQY 236

Query: 242 FED---RLAVLVDLNNGGTTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
ED R +VLV P + + T V F+C +SC M RR ++ T+E
Sbjct: 237 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 291

Query: 297 HGTLLGRKSISVKICSCPKRDMKDD 322
G +LGR+ +IC+CP RD + D+
Sbjct: 292 DGQVLGRRCFEARICACPGRDRKADE 317

☐ >gi|3695092|gb|AAC62640.1| ☒ TA*p63 beta [Mus musculus]
gi|32812142|gb|AAP87983.1| p63 TA beta [Mus musculus]
Length = 555

Score = 65.5 bits (158), Expect = 1e-09
Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
IP D+ P F+V+ + SA W YS L+KL+ + + M P
Sbjct: 165 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 224 V-IRAMPVYKKAHEVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 276 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCSNVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLLGRKSISVKICSCPKRDMKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 331 DGQVLGRRCFEARICACPGDRKDE 356

☐ >gi|1463021|gb|AAC37335.1| p53 [Canis familiaris]
 Length = 281

Score = 65.5 bits (158), Expect = 1e-09
 Identities = 46/175 (26%), Positives = 77/175 (44%), Gaps = 15/175 (8%)

Query: 152 WCYSNALEKLFVK--KKTPTVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRC-QDD 208
 W YS L KLF + K PV V+ P + +R M +Y S++ + + RC +
 Sbjct: 16 WTYSPLLNKLFQCLAKTCPVQLWVSSPPPPNTC---VRAMAIYKKSEFVTEVVRCPHHE 72

Query: 209 IAKDGAKDFAHKEHVVRCLNPDASFTGREKGVNFEDRLAVLVLDLNNGGTPQHLEKQQTVP 268
 D + A +H++R G + +DR + P + T
 Sbjct: 73 RCDSSDGLAPPQHLIRV-----EGNLRKYLDDRNTFRHSVVVPYEPPEVGSDDYTT- 124

Query: 269 VSLEFLCQNSC-PTMERRATTLVFTVENEHGTLLGRKSISVKICSCPKRDMKDD 322
 + ++C +SC M RR + T+E G +LGR S V++C+CP RD ++
 Sbjct: 125 IHNYMCNSSCMGMNRRPILTIITLEDSSGNVLGRNSFEVRVCACPGDRDRTEE 179

☐ >gi|13751181|emb|CAC37102.1| ☒ DN KET gamma protein [Rattus norvegicus]
 Length = 393

Score = 65.1 bits (157), Expect = 2e-09
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDLDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 130 V-IRAMPVYKKAHEVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 182 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCSNVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSISVKICSCPKRDMKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 237 DGQVLGRRCFEARICACPGDRKDE 262

☐ >gi|3695096|gb|AAC62642.1| ☒ DN p63 gamma [Mus musculus]
 gi|32812146|gb|AAP87987.1| p63 DN gamma [Mus musculus]
 Length = 389

Score = 65.1 bits (157), Expect = 2e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 130 V-IRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 182 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSISVKICSCPGRDMEKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 237 DGQVLGRRCFEARICACPGDRKDE 262

☐ >gi|3695098|gb|AAC62643.1| ☒ DN p63 beta [Mus musculus]
 gi|32812145|gb|AAP87986.1| p63 DN beta [Mus musculus]
 Length = 461

Score = 65.1 bits (157), Expect = 2e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 130 V-IRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVLDLNNGGTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 182 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLLGRKSISVKICSCPGRDMEKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 237 DGQVLGRRCFEARICACPGDRKDE 262

☐ >gi|13751179|emb|CAC37101.1| ☒ TA2 KET gamma protein [Rattus norvegicus]
 Length = 487

Score = 65.1 bits (157), Expect = 2e-09

Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 165 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 223

Query: 184 LKLRIIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 224 V-IRAMPVYKKAHEHVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 275

Query: 242 FED----RLAVLVLDLNNGGTTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 276 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 330

Query: 297 HGTLGRKKSISVKICSCPGRDMEKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 331 DGQVLGRRCFEARICACPGDRKRADE 356

☐ >gi|12643523|sp|Q9XSK8|P73_CERAE Tumor protein p73 (p53-like transcription factor protein)
 gi|4803650|emb|CAA72224.1| P53-like transcription factor [Cercopithecus aethiops]
 Length = 637

Score = 65.1 bits (157), Expect = 2e-09
 Identities = 57/210 (27%), Positives = 94/210 (44%), Gaps = 30/210 (14%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLF--VKKKTPVTFDVTYMQPSDY 181
 IP D+ P F V + SA W YS L+KL+ + K P+ V+ P
 Sbjct: 115 IPSNTDYPGP-HHFEVTFQSSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSAPPPPGT 173

Query: 182 SRLKLRIIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDAS-----F 233
 + +R M VY +++ + RC + ++ +D A H++R + S
 Sbjct: 174 A---IRAMPVYKKAHEVTDIVKRCPNHELGRDFNEGQSAPASHLIRVEGNLSQYVDDPV 230

Query: 234 TGREKGVNFEDRLAVLVLDLNNGGTTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFT 292
 TGR+ +V+V P + + T + F+C +SC M RR ++ T
 Sbjct: 231 TGRQ-----SVVVPYE----PPQVGTEFTT-ILYNFMCNSSCVGGMNRRPILIIIT 276

Query: 293 VENEHGTLGRKKSISVKICSCPGRDMEKDD 322
 +E G +LGR+S +IC+CP RD + D+
 Sbjct: 277 LETRDGQVLGRRSFEGRICACPGDRKRADE 306

☐ >gi|3273745|gb|AAC24830.1| ☒ p53 homolog [Homo sapiens]
 Length = 356

Score = 65.1 bits (157), Expect = 2e-09
 Identities = 55/206 (26%), Positives = 92/206 (44%), Gaps = 22/206 (10%)

Query: 125 IPVLDDFTHPLLQFNVAISGKPCSASA-WCYSNALEKLFVKKKTPVTFDVTYMQPSDYSR 183
 IP D+ P F+V+ + SA W YS L+KL+ + + M P
 Sbjct: 71 IPSNTDYPGP-HSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGA 129

Query: 184 LKLRIIMLVYSNSQYAYQTISRCQD-DIAKD-GAKDFAHKEHVVRCLNPDASFTGREKGVN 241
 + +R M VY +++ + + RC + +++++ A H++R G
 Sbjct: 130 V-IRAMPVYKKAHEHVTEVVKRCPNHELSTREFNEGQIAPPSHLIRV-----EGNSHAQY 181

Query: 242 FED----RLAVLVLDLNNGGTTPQHLEKQQTVPVSLEFLCQNSC-PTMERRATTLVFTVENE 296
 ED R +VLV P + + T V F+C +SC M RR ++ T+E
 Sbjct: 182 VEDPITGRQSVLPYE----PPQVGTEFTT-VLYNFMCNSSCVGGMNRRPILIIIVTLETR 236

Query: 297 HGTLGRKSISVKICSCPGRDMEKDD 322
 G +LGR+ +IC+CP RD + D+
 Sbjct: 237 DGQVLGRRCFEARICACPGDRKDE 262

☐ >gi|2842672|sp|Q64662|P53_SPEBE Cellular tumor antigen p53 (Tumor suppressor p53)
 gi|1165312|gb|AAA85628.1| p53
 Length = 314

Score = 65.1 bits (157), Expect = 2e-09
 Identities = 46/172 (26%), Positives = 75/172 (43%), Gaps = 14/172 (8%)

Query: 154 YSNALEKLFVK--KKTPVTFDVTYMQPSDYSRLKLRIMLVYSNSQYAYQTISRCQDDIAK 211
 YS +L KLF + K PV V P ++R M +Y SQ+ + + RC
 Sbjct: 104 YSPSLNKLFCQLAKTCPVQLWVDSTPPPG---TRVRAMAIYKKSQHMTEVVRRCPHHERC 160

Query: 212 DGAKDFAHKEHVVRCLNPDSFTGREKGVNFEDRLAVLVDLNNGGTPQHLEKQQTPVPSL 271
 + A +H++R G + +DR + P + + T +
 Sbjct: 161 SDSDGLAPPQHLIRV-----EGNLRAEYLDDRNTFRHSVVVPYEPPEVGSESTT-IHY 212

Query: 272 EFLCQNSC-PTMERRATTLVFTVENEHGTLGRKSISVKICSCPGRDMEKDD 322
 ++C +SC M RR + T+E+ G LLGR S V++C+CP RD ++
 Sbjct: 213 NYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGDRRTEE 264

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF
 Posted date: Aug 6, 2003 2:30 AM
 Number of letters in database: 478,769,834
 Number of sequences in database: 1,486,004

Lambda K H
 0.318 0.133 0.394

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 320,929,099
 Number of Sequences: 1486004
 Number of extensions: 13374429
 Number of successful extensions: 24389
 Number of sequences better than 10.0: 100
 Number of HSP's better than 10.0 without gapping: 179
 Number of HSP's successfully gapped in prelim test: 8
 Number of HSP's that attempted gapping in prelim test: 24038
 Number of HSP's gapped (non-prelim): 187
 length of query: 338
 length of database: 478,769,834

effective HSP length: 124
effective length of query: 214
effective length of database: 294,505,338
effective search space: 63024142332
effective search space used: 63024142332
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 73 (32.7 bits)

NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057859850-06894-5218

Query= SEQID32
(7 letters)

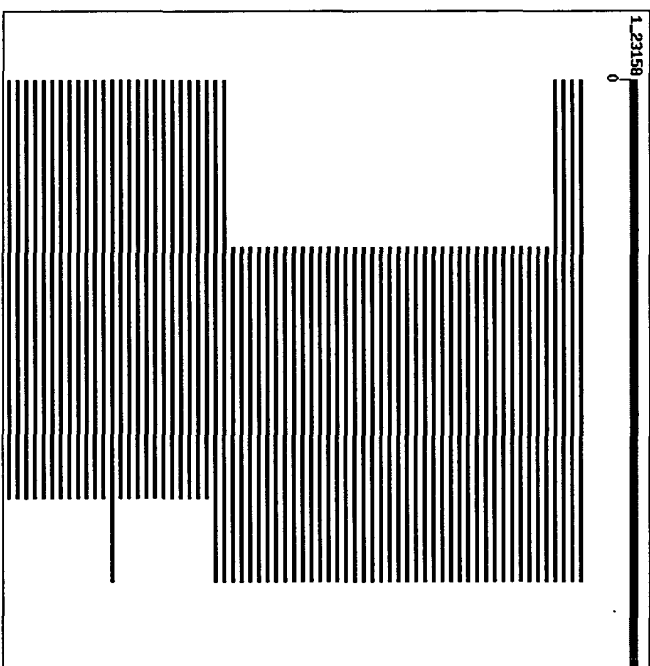
Database: All non-redundant Genbank CDS
translations+PDB+SwissProt+PIR+PRF
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQ](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

[Mouse over to show define and scores. Click to show alignments](#)



Sequences producing significant alignments:

	Score	E
	(bits)	Value
gi 32440603 emb CAA90618.2 Hypothetical protein K09A11.5 [...]	23	468
gi 21355617 ref NP_651115.1 CG10873-PA [Drosophila melanog...]	23	628
gi 25009887 gb AA071112.1 AT28346P [Drosophila melanogaster]	23	628
gi 31207283 ref XP_312608.1 ENSANGP0000014785 [Anopheles ...]	22	843
gi 27885063 gb AA026000.1 Hypothetical protein T05C3.4 [Ca...]	21	2037
gi 19909128 gb AA03124.1 AF489528.1 transforming growth fa...	21	2037
gi 19910586 ref NP_064303.1 latent transforming growth fact...	21	2037
gi 15238132 ref NP_196594.1 expressed protein [Arabidopsis...]	21	2037
gi 23008906 ref ZP_00050155.1 hypothetical protein [Magnet...]	21	2037
gi 17335887 ref NP_493679.1 Q/N-rich domain Prion like pro...	21	2037
gi 18901916 emb CA370995.1 hypothetical protein [Methanosar...]	21	2037
gi 21241370 ref NP_640952.1 hypothetical protein [Xanthomo...]	21	2037
gi 22327352 ref NP_680337.1 expressed protein [Arabidopsis...]	21	2037
gi 7506860 ref T29475 hypothetical protein T01D1.6 - Caeno...	21	2037
gi 23466945 ref ZP_00122531.1 hypothetical protein [Haemop...]	21	2037
gi 20853732 ref XP_153430.1 hypothetical protein XP_153430...	21	2037
gi 15146444 gb AA084663.1 AF351824.1 sterolin-2 [Homo sapiens]	21	2037

gi 30913084 sp O8CG19 LMBL_MOUSE	latent transforming growth...	21	2037	L
gi 25990358 gb AAAT6697.1 AF288451.1	LMBL-15 protein [Xenop...	21	2037	
gi 17565888 ref NP_504449.1	Putative plasma membrane membr...	21	2037	L
gi 14579069 gb AAK69136.1 AF280997.1	matutase K [Phyllodoctad...	21	2037	
gi 17533161 ref NP_496221.1	Cysteine rich repeat containin...	21	2037	L
gi 28499491 ref XP_144125.2	similar to KIAA1337 protein (H...	21	2037	L
gi 1756630 ref NP_506849.1	Q/N-rich domain Prion like pro...	21	2037	
gi 21227944 ref NP_633866.1	Sulfite reductase, assimilator...	21	2037	L
gi 30910081 sp O8CG18 LRBS_MOUSE	latent transforming growth...	21	2037	
gi 30352201 gb AAK1860.1	glucagon-like peptide 1 receptor...	21	2037	
gi 22537398 ref NP_688249.1	site-specific recombinase, pha...	21	2037	
gi 11967971 ref NP_071882.1	sterolin 2; Arp-binding caset...	21	2037	L
gi 23050656 ref XP_00077526.1	hypothetical protein [Methan...	21	2037	
gi 23953861 gb AAK3831.1	latent transforming growth facto...	21	2037	L
gi 15088540 gb AAK84078.1 AF324494.1	sterolin-2 (Homo sapiens)	21	2037	L
gi 14483915 gb AAK53890.1 AF280604.1	latent transforming gr...	21	2037	L
gi 17495994 pir T30136	hypothetical protein C14C11.8 - Caen...	21	2037	L
gi 17557986 ref NP_504494.1	Q/N-rich domain Prion like pro...	21	2037	L
gi 1710605 ref NP_036860.1	glucagon-like peptide 1 recepto...	21	2037	L
gi 4557731 ref NP_000618.1	latent transforming growth fact...	21	2037	L
gi 17567381 ref NP_510839.1	Predicted CDS, cysteine rich r...	21	2037	L
gi 21311480 gb AAK46745.1 AF456376.1	matutase [Phyllodoctadus...	21	2037	
gi 12505436 ref XP_192826.1	latent transforming growth fac...	21	2037	L
gi 21449820 emb CND13505.1	latent TGF-beta binding protein...	21	2037	
gi 15227656 ref NP_181183.1	hypothetical protein [Arabidop...	21	2037	
gi 17544688 ref NP_502452.1	Putative protein family member...	20	3667	L
gi 17493833 pir T05808	G protein-coupled receptor 1 - yeast...	19	6602	L
gi 27711643 ref XP_234914.1	similar to presenilin-1-like pro...	19	6602	L
gi 26353705 dbj BAC31553.1	unnamed protein product [Mus mu...	19	6602	
gi 13474878 ref NP_106448.1	nif-specific regulatory protei...	19	6602	
gi 63201701 ref NP_010249.1	G-protein-coupled receptor at p...	19	6602	
gi 30148361 ref XP_231082.2	similar to mucin [Homo sapiens]	19	6602	L
gi 12711652 ref XP_231993.1	similar to KRAZ zinc finger pr...	19	6602	L
gi 133241 sp P10281 RNZT_ASPOE	Ribonuclease T2 precursor (R...	19	6602	
gi 2350305 ref NP_701972.1	hypothetical protein [Plasmodi...	19	6602	
gi 13424359 gb AAK8721.1 AC114257.6	hypothetical protein [...	19	6602	
gi 17578395 gb AAK64095.1 AF207880.1	teashirt 2 [Mus musculus]	19	6602	L
gi 22213650 emb CAC86940.1	Iron-sulfur protein [Acidianus ...	18	11887	
gi 24266590 gb AAK52280.1 AF480620.1	phenylalanine ammonia-...	18	11887	
gi 20864524 ref XP_146397.1	similar to Putative nuclear pr...	18	11887	L
gi 23653448 ref NP_819140.1	sulfatase [Coxiella burnetii R...	18	11887	L
gi 27682355 ref XP_240891.1	hypothetical protein XP_240891...	18	11887	
gi 20218817 emb CAC84493.1	putative nucleoside diphosphate...	18	11887	
gi 14600950 ref NP_147476.1	hypothetical protein [Aetodru...	18	11887	
gi 23478566 gb AAK15617.1	hypothetical protein [Plasmodiu...	18	11887	
gi 25518475 pir T086295	hypothetical protein T24D18.16 - Ar...	18	11887	
gi 18860391 ref NP_569607.1	hypothetical protein [Psittacu...	18	11887	
gi 27666974 ref XP_224724.1	similar to hypothetical protei...	18	11887	L
gi 23987071 emb CAA16172.1	intein in MUC536.28C [Myobacte...	18	11887	
gi 16765589 ref NP_461204.1	ferredoxin-type protein: elect...	18	11887	
gi 28828206 gb AAK50887.1	hypothetical protein [Dictyoseel...	18	11887	
gi 18394319 ref NP_563990.1	ovule development protein, put...	18	11887	

gi 17563034 ref NP_503442.1	Q/N-rich domain Prion like pro...	18	11887	L
gi 15802761 ref NP_288788.1	ferredoxin-type protein: elect...	18	11887	
gi 17657281 ref NP_056623.1	keratin associated protein 5-1;...	18	11887	L
gi 32455621 ref NP_862103.1	hypothetical protein [Streptoc...	18	11887	
gi 23041377 ref XP_00072839.1	hypothetical protein [Tricho...	18	11887	
gi 21413394 ref NP_708104.1	ferredoxin-type protein: elect...	18	11887	
gi 30580804 ref NP_846617.1	expressed protein [Arabidopsis...	18	11887	
gi 22327896 ref NP_200493.2	F-box protein family [Arabidop...	18	11887	
gi 1612317 ref NP_406530.1	ferredoxin-type protein Mafp [...	18	11887	
gi 2333590 ref XP_00116849.1	hypothetical protein [Cytoph...	18	11887	
gi 29732192 ref XP_295569.1	hypothetical protein XP_295569...	18	11887	L
gi 27705140 ref XP_228089.1	similar to RUKSN cDNA 1700027D...	18	11887	L
gi 27484392 ref XP_210345.1	similar to keratin associated...	18	11887	L
gi 10176786 dbj BAK09900.1	gene_id:MK19.29-pir T01344-si...	18	11887	
gi 12619768 gb AAK60314.1 AF215129.1	conotoxin scaffold IIT...	18	11887	
gi 26248456 ref NP_754436.1	hypothetical protein [Escherich...	18	11887	
gi 29840062 ref NP_829168.1	conserved hypothetical protein...	18	11887	
gi 15827239 ref NP_301502.1	conserved hypothetical protein...	18	11887	
gi 21459391 pir S72760	protein - Mycobacterium leprae ...	18	11887	
gi 31242377 ref XP_321619.1	unnamed protein product [Mus mu...	18	11887	
gi 26334465 dbj BAC30850.1	hypothetical protein [Streptoc...	18	15950	L
gi 29822714 ref NP_822348.1	hypothetical protein [Streptoc...	18	15950	L
gi 28520318 ref XP_289380.1	hypothetical protein XP_289380...	18	15950	L
gi 17488433 pir T01524	zinc finger protein homolog T0143.2...	18	15950	
gi 29249108 gb EAA40627.1	GRP 23 41158 38234 [Gardia lamb...	18	15950	
gi 29250510 gb EAA42002.1	GRP 68 2582 684 [Gardia lambia...	18	15950	
gi 18411882 ref NP_567225.1	zinc finger protein identical...	18	15950	
gi 17533280 pir T09539	protein ANA - human >gi 3738222 dbj ...	18	15950	L
gi 1732455 ref NP_496495.1	Predicted CDS, putative endopl...	18	15950	L
gi 1314734 gb AAK9804.1	220 Kda silk protein	18	15950	
gi 15193021 gb AAK1661.1 AF378824.1	myeloid-specific perox...	18	15950	

Alignments

Get selected sequences

>gi|32440603|emb|CAA90618.2| Hypothetical protein K09A11.5 [Caenorhabditis elegans]
 Length = 650

Score = 23.1 bits (47), Expect = 468
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 FCQNSC 7
 F CQNSC
 Subject: 606 FCQNSC 612

>gi|21355617|ref|NP_651115.1| C010873-PA [Drosophila melanogaster]
 gi|17211767|gb|AAK0427.1|AF224713.1 transcription factor p53 [Drosophila melano
 gi|17211769|gb|AAK0428.1|AF224714.1 transcription factor p53 [Drosophila melano
 gi|1781624|gb|AAK61572.1|AF244918.1 p53 tumor suppressor-like protein [Drosophi

gi|8272608|gb|AA074277.1|AF250918.1 **L** transcription factor [Drosophila melanogaster]
 gi|8453116|gb|AA075270.1|AF263722.1 **L** transcription factor p53 [Drosophila melanogaster]
 gi|10726710|gb|AA056087.2| **L** CG10873-PA [Drosophila melanogaster]
 gi|17861528|gb|AA039241.1| **L** GH11591P [Drosophila melanogaster]
 gi|18032162|gb|AA056639.1|AF192555.1 p53-like regulator of apoptosis and cell cycle [Drosophila melanogaster]
 Length = 385

Score = 22.7 bits (46), Expect = 628
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 FXCONSNC 7
 F CONSNC
 Sbjct: 225 FVCONSNC 231

gi|25009887|gb|AA071112.1| AT28346p [Drosophila melanogaster]
 Length = 519

Score = 22.7 bits (46), Expect = 628
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 FXCONSNC 7
 F CONSNC
 Sbjct: 359 FVCONSNC 365

gi|31207283|ref|XP_312608.1| ENSANGP00000014785 [Anopheles gambiae]
 gi|21293812|gb|EA07957.1| ENSANGP00000014785 [Anopheles gambiae str. PEST]
 Length = 338

Score = 22.3 bits (45), Expect = 843
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 FXCONSNC 7
 F CONSNC
 Sbjct: 273 FLCCONSNC 279

gi|27885063|gb|AA026000.1| Hypothetical protein T05C3.4 [Caenorhabditis elegans]
 Length = 431

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSNC 7
 CONSNC
 Sbjct: 5 CONSNC 9

gi|13909128|gb|AA03124.1|AF489528.1 **L** transforming growth factor-beta binding
 Length = 1394

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSNC 7
 CONSNC
 Sbjct: 44 CONSNC 48

gi|9910586|ref|NP_064303.1| **L** latent transforming growth factor beta binding protein [Mus musculus]
 gi|3493176|gb|AC03307.1| **L** latent TGF beta binding protein [Mus musculus]
 Length = 1713

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSNC 7
 CONSNC
 Sbjct: 362 CONSNC 366

gi|15238132|ref|NP_196594.1| expressed protein [Arabidopsis thaliana]
 gi|11291567|ref|U50820| hypothetical protein P18022.90 - Arabidopsis thaliana
 gi|8933413|emb|CA96688.1| putative protein [Arabidopsis thaliana]
 Length = 369

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSNC 7
 CONSNC
 Sbjct: 96 CONSNC 100

gi|123008906|ref|ZP_00050155.1| hypothetical protein [Magnetospirillum magnetotacticum]
 Length = 294

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSNC 7
 CONSNC
 Sbjct: 114 CONSNC 118

gi|17535887|ref|NP_493679.1| **L** Q/N-rich domain Prion like protein PQR-61 (pqr-1) [Caenorhabditis elegans]
 gi|14574221|gb|AB037887.2| Activated in blocked unfolded protein response protein [Caenorhabditis elegans]
 Length = 395

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 3 CONSC 7
Sbjct: 202 CONSC 206

>gi|1890196|emb|CAA70995.1| hypothetical protein [Methanosarcina barkeri]
Length = 225

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 139 CONSC 143

>gi|21241370|ref|NP_640952.1| hypothetical protein [Xanthomonas axonopodis pv. c
gi|21106700|gb|AA055488.1| hypothetical protein [Xanthomonas axonopodis pv. citri]
Length = 167

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 127 CONSC 131

>gi|22327352|ref|NP_680337.1| expressed protein [Arabidopsis thaliana]
Length = 128

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 27 CONSC 31

>gi|7506860|pir||T29475 hypothetical protein T01D1.6 - Caenorhabditis elegans
Length = 411

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 218 CONSC 222

>gi|23466945|ref|ZP_00122531.1| hypothetical protein [Haemophilus somnus 129PT]
Length = 343

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 255 CONSC 259

>gi|20853732|ref|XP_153430.1| hypothetical protein XP_153430 [Mus musculus]
Length = 98

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 80 CONSC 84

>gi|15146444|gb|AA084663.1|AF351824.1 sterolin-2 [Homo sapiens]
Length = 672

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 80 CONSC 84

>gi|30913084|gb|Q8CG19|LTPB_MOUSE latent transforming growth factor beta binding
precursor (LTPB-1) (Transforming growth factor beta-1
binding protein 1) (TGF-beta1-BP-1)
gi|26006334|gb|AA077250.1| latent transforming growth factor beta binding prote
musculus]
Length = 1713

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 362 CONSC 366

>gi|25990358|gb|AA076497.1|AF288451.1 LTPB-1S protein [Xenopus laevis]
Length = 1398

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 44 CONSC 48

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

[gi|17563888|ref|NP_504449.1|](#) [L](#) Putative plasma membrane membrane protein family at least 6 transmembrane domains, nematode specific
[gi|7507180|pir|I31732](#) hypothetical protein T05C3.4 - *Caenorhabditis elegans*
 Length = 779

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
 CONSC
 Sbjct: 5 CONSC 9

[gi|14579069|gb|AAK69136.1|AF280997.1](#) maturase K [*Phyllolcladus alpinus*]
 Length = 511

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
 CONSC
 Sbjct: 183 CONSC 187

[gi|17535161|ref|NP_496221.1|](#) [L](#) Cysteine rich repeat containing protein [Caenor] [gi|75059443|pir|I73582](#) hypothetical protein M02G9.3 - *Caenorhabditis elegans*
[gi|3878599|emb|CA504626.1|](#) Hypothetical protein M02G9.3 [*Caenorhabditis elegans*]
 Length = 294

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
 CONSC
 Sbjct: 176 CONSC 180

[gi|28494921|ref|XP_144125.2|](#) [L](#) similar to KIAA1337 protein [Homo sapiens] [Mus]
 Length = 1357

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
 CONSC
 Sbjct: 582 CONSC 586

[gi|17564630|ref|NP_506849.1|](#) [L](#) Q/N-rich domain Prion like protein PQN-71 (pqn-
elegans)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

[gi|7508103|pir|T25169](#) hypothetical protein T23P1.6 - *Caenorhabditis elegans*
[gi|3880082|emb|CA503405.1|](#) C. elegans PQN-71 protein (corresponding sequence T23P
Caenorhabditis elegans)
 Length = 330

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
 CONSC
 Sbjct: 235 CONSC 239

[gi|21227944|ref|NP_633866.1|](#) Sulfite reductase, assimilatory-type [Methanosarc] [gi|20906367|gb|AAK31538.1|](#) Sulfite reductase, assimilatory-type [Methanosarcina m
 Length = 224

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
 CONSC
 Sbjct: 138 CONSC 142

[gi|30913083|sp|Q8CG18|LTHS_MOUSE](#) Latent transforming growth factor beta binding
 IS precursor (LTHP-1) (Transforming growth factor
 beta-1 binding protein 1) (TGF-beta1-BP-1)
[gi|26006335|gb|AA77251.1|](#) latent transforming growth factor beta binding protein
 musculus)
 Length = 1389

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
 CONSC
 Sbjct: 39 CONSC 43

[gi|30352201|gb|AAFP31860.1|](#) glucagon-like peptide 1 receptor [GLP-1 receptor [Rat]
 Length = 463

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
 CONSC
 Sbjct: 458 CONSC 462

[gi|22537398|ref|NP_688249.1|](#) site-specific recombinase, phage integrase family
agalactiae 2603V/R1
[gi|22534273|gb|AA00122.1|AB014249.3](#) site-specific recombinase, phage integrase f
agalactiae 2603V/R1

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Length = 399

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)Query: 3 CONSC 7
CONSC
Sbjct: 391 CONSC 395

[gi|11967971|ref|NP_071882.1|](#) **1** sterolin 2; ATP-binding cassette, subfamily G, **1**
[sapiens](#)
[gi|17432916|sp|Q9H221|ABG8_HUMAN](#) **1** ATP-binding cassette, sub-family G, member 8 (**1**)
[gi|11692802|gb|AA640004.1|AF320294.1](#) **1** ABCG8 (Homo sapiens)
 Length = 673

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)Query: 3 CONSC 7
CONSC
Sbjct: 80 CONSC 84

[gi|23050656|ref|ZP_00077526.1|](#) hypothetical protein [Methanosarcina barkeri]
 Length = 228

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)Query: 3 CONSC 7
CONSC
Sbjct: 142 CONSC 146

[gi|23953861|gb|AA38831.1|](#) **1** latent transforming growth factor beta binding pr
[musculus](#)
 Length = 55

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)Query: 3 CONSC 7
CONSC
Sbjct: 25 CONSC 29

[gi|15088540|gb|AA84078.1|AF324494.1](#) **1** sterolin-2 (Homo sapiens)
 Length = 673

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

CONSC
Sbjct: 80 CONSC 84

[gi|12483915|gb|AA653890.1|AF280604.1](#) **1** latent transforming growth factor beta **1**
[precursor \(Mus musculus\)](#)
 Length = 165

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)Query: 3 CONSC 7
CONSC
Sbjct: 44 CONSC 48

[gi|7495994|pir|T30136](#) hypothetical protein C14C11.8 - Caenorhabditis elegans
 Length = 654

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)Query: 3 CONSC 7
CONSC
Sbjct: 556 CONSC 560

[gi|17557986|ref|NP_504494.1|](#) **1** Q/N-rich domain Prion like protein PGN-13 (70.0
[\[Caenorhabditis elegans\]](#)
[gi|14573802|gb|AA96110.2|](#) Prion-like (Q/N-rich)-domain-bearing protein 1
[\[Caenorhabditis elegans\]](#)
 Length = 661

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)Query: 3 CONSC 7
CONSC
Sbjct: 563 CONSC 567

[gi|7110605|ref|NP_036860.1|](#) **1** glucagon-like peptide 1 receptor; Pancreatic bet
[\[Rattus norvegicus\]](#)
[gi|417070|sp|P32301|GLP1_RAT](#) Glucagon-like peptide 1 receptor precursor (GLP-1 re
[\(GLP-1-R\)](#)
[gi|423852|pir|A46172](#) glucagon-like peptide 1 receptor - rat
[gi|387868|gb|AA73377.1|](#) **1** [rat mRNA sequence.], gene product
 Length = 463

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

CONSC
Sbjct: 458 CONSC 462

[>gi|4557731|ref|NP_000618.1|] [L] latent transforming growth factor beta binding precursor [Homo sapiens]
gi|135691|sp|P22064|LTHS_HUMAN latent transforming growth factor beta binding precursor (LTBP-1) (Transforming growth factor beta-1 binding protein 1) (TGF-beta1-BP-1)
gi|107945|pir|I35626 transforming growth factor beta-1 binding protein - human
gi|339548|gb|AA61160.1| [L] transforming growth factor-beta 1 binding protein precursor
Length = 1394

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 44 CONSC 48

[>gi|17567385|ref|NP_510839.1|] [L] Predicted CDS, cysteine rich repeat containing member [Caenorhabditis elegans]
gi|7500204|pir|T26599 hypothetical protein F31A3.1 - Caenorhabditis elegans
gi|1326321|gb|AAH36856.1| Hypothetical protein F31A3.1 [Caenorhabditis elegans]
Length = 242

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 117 CONSC 121

[>gi|21311480|gb|AAW46745.1|AF456376.1] maturase [Phyllolcladus trichomanoides]
Length = 511

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 183 CONSC 187

[>gi|25054368|ref|XP_192826.1|] [L] latent transforming growth factor beta binding I musculus
Length = 1520

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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CONSC
Sbjct: 169 CONSC 173

[>gi|21449820|emb|CAD3505.1|] latent TGF-beta binding protein 1 [Xenopus laevis]
Length = 1399

Score = 21.0 bits (42), Expect = 2037
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CONSC 7
Sbjct: 44 CONSC 48

[>gi|15227656|ref|NP_181183.1|] hypothetical protein [Arabidopsis thaliana]
gi|25408473|pir|E84780 hypothetical protein AC2936420 [imported] - Arabidopsis thaliana
gi|4581142|gb|AAD24626.1| unknown protein [Arabidopsis thaliana]
Length = 439

Score = 20.6 bits (41), Expect = 2733
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 1 FXCONSC 7
Sbjct: 57 FSCNSC 63

[>gi|17544688|ref|NP_502452.1|] [L] Putative protein family member, nematode specific [elegans]
gi|7511394|pir|T28079 hypothetical protein ZK896.1 - Caenorhabditis elegans
gi|3881865|emb|CAH05322.1| Hypothetical protein ZK896.1 [Caenorhabditis elegans]
Length = 410

Score = 20.2 bits (40), Expect = 3667
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 1 FXCONSC 7
Sbjct: 187 FSCNSC 193

[>gi|7493833|pir|JC5808] G protein-coupled receptor 1 - yeast [Saccharomyces cerevisiae]
Length = 962

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
Sbjct: 458 FSCONS 463

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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☐ >gi|27177663|ref|XP_234914.1| **L** similar to presentin-like protein 1 [Homo sapiens] norvegicus]
Length = 1759

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
F CONS
Sbjct: 859 FSCONS 864

☐ >gi|26335705|dbj|BAC31553.1| unnamed protein product [Mus musculus]
gi|28913719|gb|AAH48570.1| Similar to protein tyrosine phosphatase, receptor type polypeptide 2 [Mus musculus]
Length = 118

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
F CONS
Sbjct: 108 FSCONS 113

☐ >gi|13474878|ref|NP_106448.1| nif-specific regulatory protein, nifA [Mesorhizobium gi|14026363|dbj|BA852334.1| nif-specific regulatory protein; NifA [Mesorhizobium]
Length = 583

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
F CONS
Sbjct: 466 FSCONS 471

☐ >gi|6320170|ref|NP_010249.1| G-protein-coupled receptor at plasma membrane; inte two-hybrid system with Gpa2p; Gpr1p [Saccharomyces cerevisiae]
gi|26394417|sp|O12361|GPRL YEAST G protein-coupled receptor GPRL
gi|2132416|pif|J567568 probable membrane protein YDL035c - yeast (Saccharomyces cerevisiae)
gi|1279681|emb|CA96454.1| unknown [Saccharomyces cerevisiae]
gi|1431015|emb|CA98593.1| ORF YDL035c [Saccharomyces cerevisiae]
Length = 961

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
F CONS
Sbjct: 457 FSCONS 462

☐ >gi|3014365|ref|XP_293082.2| **L** similar to mucin [Homo sapiens] norvegicus]
Length = 1293

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
F CONS
Sbjct: 917 FSCONS 922

☐ >gi|2711652|ref|XP_231993.1| **L** similar to KRAB zinc finger protein 6D [Mus mus norvegicus]
Length = 303

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCONS 6
F CONS
Sbjct: 99 FSCONS 104

Get selected sequences Selected all Deselect all

Database: All non-redundant GenBank CDS
Translations+PDB+SwissProt+PIR+PFR
Posted date: Jul 10, 2003 1:49 AM
Number of letters in database: 474,244,320
Number of sequences in database: 1,477,204

Lambda K H
0.362 0.277 2.25
Gapped
Lambda K H
0.294 0.110 0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of Hits to DB: 3,712,852
Number of Sequences: 1477204
Number of Extensions: 5677
Number of successful extensions: 129
Number of sequences better than 20000.0: 100
Number of HSP's better than 20000.0 without gapping: 129
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Length of query: 7
Length of database: 474,244,320
Effective HSP length: 0
Effective length of query: 9

RID=1057859830-06894-5218, SEQID32

Page 17 of 17

effective length of database: 474,244,320
effective search space: 426819880
effective search space used: 426819880
T: 11
A: 40
X1: 14 (7.3 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 35 (20.1 bits)
S2: 35 (18.0 bits)



EXHIBIT F

RID=1057861440-028425-7091, SEQID23

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RID=1057861440-028425-7091, SEQID23

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NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057861440-028425-7091

Query: SEQID23
(9 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

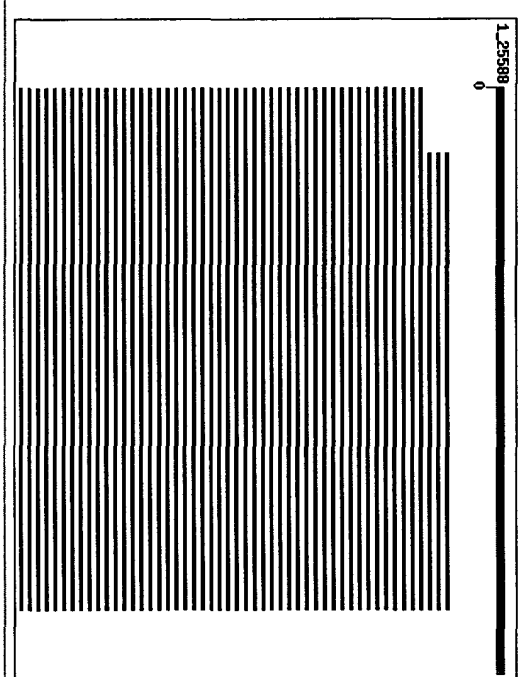
[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments

<http://www.ncbi.nlm.nih.gov/blast/blast.cgi>

7/10/2003



Sequences producing significant alignments:		Score	E
		(bits)	Value
gi 31207283 ref XP_312608.1	ENSANGP00000014785 (Anopheles ...	31	2.4
gi 21355617 ref NP_651115.1	CG10873-PA (Drosophila melanog...	28	14
gi 25009887 gb AA071112.1	AT28346p (Drosophila melanogaster)	28	14
gi 3695096 gb AAC62642.1	DN p63 gamma (Mus musculus)	26	80
gi 13751181 emb CAC37102.1	DN KET gamma protein (Rattus no...	26	80
gi 13751173 emb CAC37098.1	TAL KET alpha protein (Rattus n...	26	80
gi 20428532 gb AAK81886.1	DN p73 gamma (Homo sapiens)	26	80
gi 1813455 gb AAB41833.1	p53	26	80
gi 19909983 dbj BAB87245.1	deltan p73 beta (Homo sapiens) ...	26	80
gi 7248451 gb AAF43492.1	p51 isoform delnbeta (Homo sapiens)	26	80
gi 20892181 ref XP_147232.1	transformation related protein...	26	80
gi 3695094 gb AAC62641.1	TA*P63 alpha (Mus musculus)	26	80
gi 12060406 dbj BAB20591.1	delta N p73L (Homo sapiens)	26	80
gi 4803651 emb CAA72225.1	p73 splice variant (Carcopithec...	26	80
gi 13751179 emb CAC37101.1	TA2 KET gamma protein (Rattus n...	26	80
gi 15072750 emb CAC48053.1	p63 delta (Homo sapiens)	26	80
gi 29470179 gb AA074632.1	p73 (Danio rerio)	26	80
gi 2581764 gb AAB82420.1	p53 (Cricetus griseus)	26	80
gi 8217464 emb CAB92742.1	dT1092A11.2 (tumor protein p73) ...	26	80
gi 23701781 emb CAA72221.1	second splice variant (Homo sapi...	26	80
gi 21264484 sp P79820 P53	ORXLA Cellular tumor antigen p53 ...	26	80
gi 1184759 gb AA87577.1	p53 tumor suppressor homolog	26	80
gi 1184757 gb AA87576.1	p53 tumor suppressor homolog	26	80
gi 7248450 gb AAF43491.1	p51 isoform delnalpha (Homo sapiens)	26	80

<http://www.ncbi.nlm.nih.gov/blast/blast.cgi>

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gi 17248447 gb AAAF4348.1	p51 isoform TAP63beta [Homo sapiens]	26	80
gi 13273745 gb AAC24830.1	p53 homolog [Homo sapiens]	26	80
gi 473379 gb AAAB1344.1	tumor suppressor p53 [Mesocricetus ...]	26	80
gi 27527178 emb CAD0682.1	p53 protein [Monodelphis domestica]	26	80
gi 12024746 gb AAAG45609.1	TA p63 gamma [Homo sapiens]	26	80
gi 3695098 gb AAC62643.1	DN p63 beta [Mus musculus]	26	80
gi 4685086 gb AA027752.1	AF043641.1 p73 [Barbus barbus]	26	80
gi 6755883 ref NP_035771.1	transformation related protein ...	26	80
gi 1244762 gb AAAG9863.1	p53 tumor suppressor homolog	26	80
gi 13751175 emb CAC37105.1	DN KET beta protein [Rattus nor...	26	80
gi 13751175 emb CAC37099.1	DN KET alpha protein [Rattus no...	26	80
gi 23308709 ref NP_694518.1	deltap63 isoform alpha 1; tum...	26	80
gi 26339452 dbj BAC33397.1	unnamed protein product [Mus mu...	26	80
gi 23308711 ref NP_694519.1	deltap63 isoform gamma; tumor...	26	80
gi 3695082 gb AAC62635.1	TA p63 alpha [Homo sapiens]	26	80
gi 1698502 gb AAC60146.1	p53 [Oryzias latipes] >gi 1208249...	26	80
gi 20850793 ref XP_131858.1	transformation related protein...	26	80
gi 13195250 gb AAK15622.1	AF314148.1 p63 DNA binding protei...	26	80
gi 3510328 dbj BAJ32592.1	p51A [Homo sapiens] >gi 3695078 ...	26	80
gi 13751185 emb CAC37104.1	TA1 KET beta protein [Rattus no...	26	80
gi 1813453 db AAAB1832.1	tumor suppressor protein [Mesocric...	26	80
gi 3695080 gb AAC62634.1	p53	26	80
gi 1813453 gb AAAB1831.1	DN p63 gamma [Homo sapiens] >gi 7...	26	80
gi 3970717 emb CAA76662.1	KET protein [Homo sapiens]	26	80
gi 123308685 ref NP_689454.1	deltap63 isoform alpha 2; tum...	26	80
gi 13445484 dbj BAJ32433.1	p73H [Homo sapiens]	26	80
gi 17689271 gb AAE67733.1	AF253323.1 p53 tumor suppressor-1...	26	80
gi 17985367 gb AA50211.1	tumor protein [Canis familiaris]	26	80
gi 31543818 ref NP_003713.3	tumor protein p73-like; tumor ...	26	80
gi 19909991 dbj BAH67244.1	deltap63 alpha [Homo sapiens]...	26	80
gi 4101546 gb AAAD0196.1	tumor suppressor protein p53 [Ory...	26	80
gi 1813457 gb AAAB1834.1	p53	26	80
gi 1244764 gb AAAG9864.1	p53 tumor suppressor homolog	26	80
gi 7440008 dbj CC6176	tumor suppressor protein p53 - Chine...	26	80
gi 1286666 dbj BAH30732.1	unnamed protein product [Mus mu...	26	80
gi 19850152 gb AAE9584.1	AF285104.1 p53-like transfection...	26	80
gi 17320915 emb CAB81954.1	p73 delta-N protein [Mus musculus]	26	80
gi 1293701 gb U003661 p53_KFSNU	Cellular tumor antigen p53 (T...	26	80
gi 17689273 gb AAE67734.1	AF253324.1 p73-like protein [Mya a...	26	80
gi 3695088 gb AAC62638.1	DN p63 beta [Homo sapiens] >gi 12...	26	80
gi 3370177 emb CAA72219.1	first splice variant [Homo sapiens]	26	80
gi 3510330 dbj BAJ32593.1	p51B [Homo sapiens] >gi 7248446 ...	26	80
gi 18903327 emb CAA7109.1	p53 tumor suppressor [Cricetulu...	26	80
gi 17248447 gb AAAF4349.1	p51 isoform delta [Homo sapiens]	26	80
gi 1206467 dbj BAH20631.1	DN p63 alpha [Gallus gallus]	26	80
gi 3695092 gb AAC62640.1	TA*p63 beta [Mus musculus]	26	80
gi 10720194 sp IPRTAL1 P53_TURGB	Cellular tumor antigen p53 ...	26	80
gi 17248446 gb AAAF4348.1	p51 isoform TAP63delta [Homo sapi...	26	80
gi 3695090 gb AAC62639.1	TA*p63 gamma [Mus musculus]	26	80
gi 2499428 gb U009185 P53_CRIGR	Cellular tumor antigen p53 (...)	26	80
gi 12643523 sp Q9YSK8 P73_CERAR	Tumor protein p73 (p53-like)...	26	80

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi

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gi 4885645 ref NP_005418.1	tumor protein p73; p53-related ...	26	80
gi 12024745 gb AAAG45608.1	TA p63 beta [Homo sapiens]	26	80
gi 9507209 ref NP_062094.1	transformation related protein ...	26	80
gi 3695086 gb AAC62637.1	TA p63 beta [Homo sapiens]	26	80
gi 4887145 gb AAJ32213.1	p73 [Mus musculus]	26	80
gi 13751183 emb CAC37103.1	TA2 KET beta protein [Rattus no...	26	80
gi 3644040 gb AAC43038.1	CUSP [Homo sapiens] >gi 3695084 g...	26	80
gi 13751177 emb CAC37100.1	TA1 KET gamma protein [Rattus n...	26	80
gi 12386780 gb BAC21014.1	claudin42 [Xenopus laevis]	25	144
gi 17559712 ref NP_506256.1	Cadherin protein like [Caenorh...	24	194
gi 27705398 ref XP_230942.1	similar to dufs102.1.1 (Cadher...	24	194
gi 28071273 dbj BAC55566.1	tumor necrosis factor receptor...	24	194
gi 121623719 gb BAC00941.1	HT-protein [Lycopersicon peruvi...	24	260
gi 17227039 gb AAK137982.1	AF442140.1 style-specific self-in...	24	260
gi 121623726 dbj BAC00944.1	HT-A protein [Lycopersicon chi...	24	260
gi 12313187 ref ZP_00098587.1	hypothetical protein [Desulf...	24	260
gi 30039744 ref NP_835472.1	rolling circle replication pro...	24	260
gi 21623723 dbj BAC00943.1	HT-protein [Lycopersicon parvif...	24	260
gi 21623729 dbj BAC00945.1	HT-A protein [Lycopersicon hirs...	24	260
gi 17227037 gb AAK137981.1	AF442139.1 style-specific self-in...	24	260
gi 152188576 ref NP_174690.1	expressed protein [Arabidopsis...	24	349
gi 1293712 sp P10361 P53_RAT	Cellular tumor antigen p53 (Tum...	23	468
gi 7259331 dbj BAH92786.1	p53 [Macaca fasciata]	23	468
gi 693787 gb AAJ31269.1	tumor suppressor [Canis familiaris]	23	468

Alignments

Get selected sequences	Select all	Deselect all
------------------------	------------	--------------

Query: 2 ICSCPRD 9
 Subject: 310 ICSCPRD 317
 Score = 30.8 bits (65), Expect = 2.4
 Identities = 8/8 (100%), Positives = 8/8 (100%)
 Length = 338

gi 131207283 ref XP_312608.1	ENSANGP00000014785 [Anopheles gambiae]
gi 12193812 gb BAH07557.1	ENSANGP00000014785 [Anopheles gambiae str. PGST]
Length = 338	
Score = 30.8 bits (65), Expect = 2.4	
Identities = 8/8 (100%), Positives = 8/8 (100%)	
Query: 2 ICSCPRD 9	
Subject: 310 ICSCPRD 317	
gi 21335617 ref NP_651115.1	CG10873-PA [Drosophila melanogaster]
gi 17211567 gb AAAF40427.1	AF224773.1 transcription factor p53 [Drosophila melano]
gi 17211569 gb AAAF40428.1	AF224774.1 transcription factor p53 [Drosophila melano]
gi 17331624 gb AAAF61572.1	AF244918.1 p53 tumor suppressor-like protein [Drosophi]
gi 8272608 gb AAAF4277.1	AF250918.1 transcription factor [Drosophila melanogast]
gi 8453176 gb AAAF75270.1	AF263722.1 transcription factor p53 [Drosophila melano]
gi 10726710 gb AAAF6087.2	CG10873-PA [Drosophila melanogaster]
gi 17861528 gb AAJ39241.1	GH11591p [Drosophila melanogaster]

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi

7/10/2003

gi|18032162|gb|AA156639.1|AF192555.1 p53-like regulator of apoptosis and cell cycle
melanogaster]

Length = 385

Score = 28.2 bits (59), Expect = 14
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 2 ICSCPRD 9

IC+CP RD
Sbjct: 260 ICRCPRD 267

gi|25009887|gb|AA171112.1| AT28346p [Drosophila melanogaster]
Length = 519

Score = 28.2 bits (59), Expect = 14
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 2 ICSCPRD 9

IC+CP RD
Sbjct: 394 ICRCPRD 401

gi|3695096|gb|AA62642.1| DN p63 gamma [Mus musculus]
Length = 389

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPRD 9

RIC+CP RD
Sbjct: 249 RICACPRD 257

gi|13751181|emb|CAC37102.1| DN KRT gamma protein [Rattus norvegicus]
Length = 393

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPRD 9

RIC+CP RD
Sbjct: 249 RICACPRD 257

gi|13751173|emb|CAC37098.1| TAI KRT alpha protein [Rattus norvegicus]
Length = 663

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPRD 9

RIC+CP RD
Sbjct: 326 RICACPRD 334

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

gi|20428532|gb|AAK81886.1| DN p73 gamma [Homo sapiens]
Length = 426

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPRD 9

RIC+CP RD
Sbjct: 244 RICACPRD 252

gi|1813455|gb|AAK1833.1| p53
Length = 238

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPRD 9

RIC+CP RD
Sbjct: 166 RICACPRD 174

gi|19909983|dbj|BA87245.1| deltan p73 beta [Homo sapiens]
gi|20428530|gb|AAK81885.1| DN p73 beta [Homo sapiens]
Length = 450

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPRD 9

RIC+CP RD
Sbjct: 244 RICACPRD 252

gi|2248451|gb|AAE43492.1| p51 isoform delnbeta [Homo sapiens]
Length = 461

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPRD 9

RIC+CP RD
Sbjct: 249 RICACPRD 257

gi|20892181|ref|XP_147232.1| transformation related protein 63 [Mus musculus]
Length = 465

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPRD 9

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

RIC+CP RD
Sbjct: 128 RICACPRND 136

[\[>gi|3695094|gb|AAC62641.1\]](#) **TA**p63 alpha [Mus musculus]
Length = 680

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCPRND 9
RIC+CP RD
Sbjct: 343 RICACPRND 351

[\[>gi|12060406|dbj|BAB20591.1\]](#) delta N p73L [Homo sapiens]
Length = 501

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCPRND 9
RIC+CP RD
Sbjct: 164 RICACPRND 172

[\[>gi|4803651|emb|CAA72225.1\]](#) p73 splice variant [Cercopithecus aethiops]
Length = 495

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCPRND 9
RIC+CP RD
Sbjct: 293 RICACPRND 301

[\[>gi|13751179|emb|CAC37101.1\]](#) **TA2** KET gamma protein [Rattus norvegicus]
Length = 487

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCPRND 9
RIC+CP RD
Sbjct: 343 RICACPRND 351

[\[>gi|15072750|emb|CAC48053.1\]](#) p63 delta [Homo sapiens]
Length = 232

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 1 RISCPRND 9
RIC+CP RD
Sbjct: 191 RICACPRND 199

[\[>gi|29470179|gb|AA074632.1\]](#) p73 [Danio rerio]
Length = 640

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCPRND 9
RIC+CP RD
Sbjct: 300 RICACPRND 308

[\[>gi|2581764|gb|AA82420.1\]](#) p53 [Cricetulus griseus]
Length = 205

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCPRND 9
RIC+CP RD
Sbjct: 148 RICACPRND 156

[\[>gi|8217484|emb|CA92742.1\]](#) dJ1092A11.2 (tumor protein p73) [Homo sapiens]
Length = 661

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCPRND 9
RIC+CP RD
Sbjct: 318 RICACPRND 326

[\[>gi|2370178|emb|CAA72221.1\]](#) **TA** second splice variant [Homo sapiens]
Length = 588

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RISCPRND 9
RIC+CP RD
Sbjct: 245 RICACPRND 253

[\[>gi|21264484|sp|P79820|P53_ORYLA\]](#) Cellular tumor antigen p53 (Tumor suppressor p53) [Oryzias latipes]
[gi|4101544|gb|AAD01195.1\]](#) tumor suppressor protein p53 [Oryzias latipes]
Length = 352

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 25.7 bits (53), Expect = 80
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPKRD 9
 RIC+CP RD
 Sbjct: 254 R1CACPKGRD 262

[->gi|1184759|gb|AA87577.1| p53 tumor suppressor homolog
 Length = 189

Score = 25.7 bits (53), Expect = 80
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPKRD 9
 RIC+CP RD
 Sbjct: 89 R1CACPKGRD 97

[->gi|1184757|gb|AA87576.1| p53 tumor suppressor homolog
 Length = 228

Score = 25.7 bits (53), Expect = 80
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPKRD 9
 RIC+CP RD
 Sbjct: 97 R1CACPKGRD 105

[->gi|7248450|gb|AA743491.1| p51 isoform delNalpha [Homo sapiens]
 Length = 586

Score = 25.7 bits (53), Expect = 80
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPKRD 9
 RIC+CP RD
 Sbjct: 249 R1CACPKGRD 257

[->gi|7248447|gb|AA743488.1| p51 isoform T9p63beta [Homo sapiens]
 Length = 516

Score = 25.7 bits (53), Expect = 80
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPKRD 9
 RIC+CP RD
 Sbjct: 304 R1CACPKGRD 312

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

[->gi|3273745|gb|AAC24830.1| p53 homolog [Homo sapiens]
 Length = 356

Score = 25.7 bits (53), Expect = 80
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPKRD 9
 RIC+CP RD
 Sbjct: 249 R1CACPKGRD 257

[->gi|473579|gb|AA81344.1| tumor suppressor p53 [Mesocricetus auratus]
 Length = 396

Score = 25.7 bits (53), Expect = 80
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPKRD 9
 RIC+CP RD
 Sbjct: 276 R1CACPKGRD 284

[->gi|27527178|emb|CADI0682.1| p53 protein [Monodelphis domestica]
 Length = 238

Score = 25.7 bits (53), Expect = 80
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPKRD 9
 RIC+CP RD
 Sbjct: 145 R1CACPKGRD 153

[->gi|12024746|gb|MG45609.1| p53 gamma [Homo sapiens]
 Length = 487

Score = 25.7 bits (53), Expect = 80
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPKRD 9
 RIC+CP RD
 Sbjct: 343 R1CACPKGRD 351

[->gi|3695098|gb|AAC62643.1| DN p63 beta [Mus musculus]
 Length = 461

Score = 25.7 bits (53), Expect = 80
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPKRD 9
 RIC+CP RD
 Sbjct: 249 R1CACPKGRD 257

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

>gi|4689086|gb|AA027752.1|AF043641.1 p73 [Barbus barbus]
Length = 641

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRND 9
R1C+CP RD
Sbjct: 301 R1CACPRND 309

>gi|6755883|ref|NP_035771.1| L transformation related protein 63; KET protein; t
[Mus musculus]

gi|3445482|dbj|BA32432.1| L p73H [Mus musculus]
gi|3695100|gb|AAC62644.1| L DN p63 alpha [Mus musculus]
Length = 586

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRND 9
R1C+CP RD
Sbjct: 249 R1CACPRND 257

>gi|1244762|gb|AA93563.1| p53 tumor suppressor homolog
Length = 564

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRND 9
R1C+CP RD
Sbjct: 238 R1CACPRND 306

>gi|13751187|emb|CAC37105.1| L DN KET beta protein [Rattus norvegicus]
Length = 461

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRND 9
R1C+CP RD
Sbjct: 249 R1CACPRND 257

>gi|13751175|emb|CAC37099.1| L DN KET alpha protein [Rattus norvegicus]
Length = 586

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

Query: 1 R1CSCPRND 9
R1C+CP RD
Sbjct: 249 R1CACPRND 257

>gi|23308709|ref|NP_694518.1| L deltaNp63 isoform alpha 1; tumor protein p63 [D
gi|22652331|gb|AA03690.1|AF412283.1 L DN p63 alpha 1 [Danio rerio]
Length = 588

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRND 9
R1C+CP RD
Sbjct: 247 R1CACPRND 255

>gi|2639452|dbj|BAC33397.1| unnamed protein product [Mus musculus]
Length = 284

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRND 9
R1C+CP RD
Sbjct: 249 R1CACPRND 257

>gi|23308711|ref|NP_694519.1| L deltaNp63 isoform gamma; tumor protein p63 [Dan
gi|22652335|gb|AA03692.1|AF412285.1 L DN p63 gamma [Danio rerio]
Length = 457

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRND 9
R1C+CP RD
Sbjct: 247 R1CACPRND 255

>gi|3695082|gb|AAC62635.1| L TA p63 alpha [Homo sapiens]
Length = 641

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRND 9
R1C+CP RD
Sbjct: 304 R1CACPRND 312

>gi|1698502|gb|AAC60146.1| p53 [Oryzias latipes]

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

[gi|12082495|gb|AA048557.1|AF212997.1](#) p53 tumor suppressor (Oryzias latipes)
Length = 351

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRD 9
RIC+CP RD
Sbjct: 253 R1CACPRD 261

[gi|20850793|ref|XP_111858.1](#) transformation related protein 73 [Mus musculus]
[gi|30794514|ref|NP_035772.1](#) transformation related protein 73 [Mus musculus]
[gi|15209244|emb|CA881953.1](#) p73 alpha protein [Mus musculus]
Length = 631

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRD 9
RIC+CP RD
Sbjct: 285 R1CACPRD 293

[gi|113195250|gb|AAK15622.1|AF314148.1](#) p63 DNA binding protein [Xenopus laevis]
Length = 365

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRD 9
RIC+CP RD
Sbjct: 249 R1CACPRD 257

[gi|3510328|dbj|BA032992.1](#) p51A [Homo sapiens]
[gi|3695078|gb|AAC62633.1](#) TA p63 gamma [Homo sapiens]
[gi|7240445|gb|AA043486.1](#) p51 isoform TP63gamma [Homo sapiens]
Length = 448

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRD 9
RIC+CP RD
Sbjct: 304 R1CACPRD 312

[gi|113751185|emb|CAC37104.1](#) TAI KET beta protein [Rattus norvegicus]
Length = 538

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 1 R1CSCPRD 9
RIC+CP RD
Sbjct: 326 R1CACPRD 334

[gi|451931|gb|AA37086.1](#) tumor suppressor protein [Mesocricetus auratus]
Length = 206

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRD 9
RIC+CP RD
Sbjct: 148 R1CACPRD 156

[gi|1813451|gb|AA041832.1](#) p53
Length = 286

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRD 9
RIC+CP RD
Sbjct: 166 R1CACPRD 174

[gi|3695080|gb|AAC62634.1](#) DN p63 gamma [Homo sapiens]
[gi|7248443|gb|AA043490.1](#) p51 isoform delngamma [Homo sapiens]
[gi|12024749|gb|AA045612.1](#) DN p63 gamma [Homo sapiens]
Length = 393

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRD 9
RIC+CP RD
Sbjct: 249 R1CACPRD 257

[gi|1813451|gb|AA041832.1](#) p53
Length = 378

Score = 25.7 bits (53), Expect = 80
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 R1CSCPRD 9
RIC+CP RD
Sbjct: 258 R1CACPRD 266

[gi|3970717|emb|CAA76562.1](#) KET protein [Homo sapiens]
Length = 680

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 25.7 bits (53), Expect = 80
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPKRD 9
 RIC+CP RD
 Subject: 343 RICACPKRD 351

gi|23308685|ref|NP_689454.1| **1** deltanp63 isoform alpha 2; tumor protein p63 [D
 gi|21326973|gb|AA048108.1|AF487944.1 **2** deltan p63 alpha [Danio rerio]
 gi|22652333|gb|AA003691.1|AF412284.1 **3** DN p63 alpha 2 [Danio rerio]
 Length = 576

Score = 25.7 bits (53), Expect = 80
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RICSCPKRD 9
 RIC+CP RD
 Subject: 247 RICACPKRD 255

Get selected sequences

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PPF
 Posted date: Jul 10, 2003 1:49 AM
 Number of letters in database: 474,244,320
 Number of sequences in database: 1,477,204

Lambda K H
 0.355 0.291 2.09

Gapped
 Lambda K H
 0.294 0.110 0.610

Matrix: PAM30
 Gap Penalties: Existence: 9, Extension: 1
 Number of Hits to DB: 7,787,423
 Number of Sequences: 1477204
 Number of extensions: 37039
 Number of successful extensions: 1121
 Number of sequences better than 20000.0: 100
 Number of HSP's better than 20000.0 without gapping: 1073
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1121
 length of query: 9
 length of database: 474,244,320
 effective HSP length: 0
 effective length of query: 9
 effective length of database: 474,244,320

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

effective search space: 4268198880
 effective search space used: 4268198880
 T: 11
 A: 40
 X1: 14 (7.2 bits)
 X2: 35 (14.8 bits)
 X3: 58 (24.6 bits)
 S1: 35 (19.7 bits)
 S2: 35 (18.0 bits)

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

NCBI

results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

RID: 1057861369-027523-7419

Query: SEQID24

(9 letters)

Database: All non-redundant Genbank CDS
translations+PDB+SwissProt+PIR+PP
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQ](#)

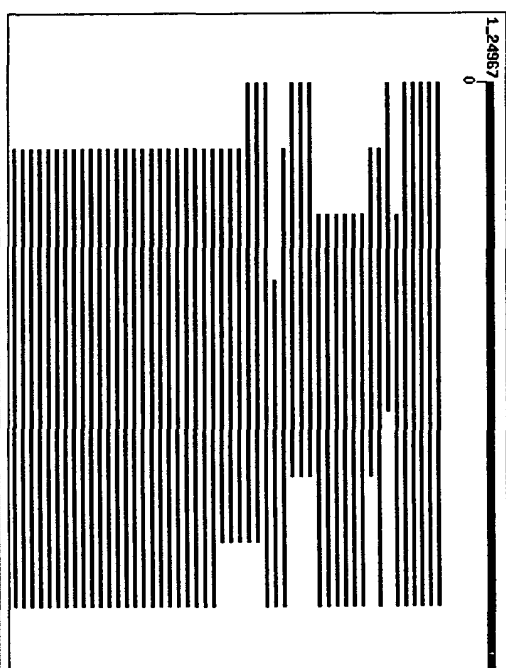
[Taxonomy reports](#)

Distribution of 113 Blast Hits on the Query Sequence

[Mouse-over to show define and scores](#) [Click to show alignments](#)<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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EXHIBIT G



Sequences producing significant alignments:

	Score	E
	(bits)	Value
gi 31207283 ref XP_312608.1 ENSANGP00000014785 [Anopheles ...	34	0.30
gi 21355617 ref NP_651115.1 Cg10873-PA [Drosophila melanogaster]...	31	1.8
gi 25009887 gb AA071112.1 AT28346P [Drosophila melanogaster]	31	1.8
gi 1673504 emb CA66181.1 G protein-coupled receptor kinase...	26	60
gi 12621084 ref NP_075217.1 G protein-coupled receptor kin...	26	60
gi 23867780 db BAC21014.1 claudin4L2 [Xenopus laevis]	25	144
gi 21623719 db BAC00941.1 HT-protein [Lycopersicon peruv...	24	260
gi 17227039 db AA137982.1 AF442140.1 style-specific self-in...	24	260
gi 21623726 db BAC00944.1 HT-A protein [Lycopersicon chm...	24	260
gi 123113187 ref ZP_00098587.1 hypothetical protein [Desulf...	24	260
gi 30039744 ref NP_835472.1 rolling circle replication pro...	24	260
gi 29565659 ref NP_817241.1 ORP82 [Pinus koraiensis] >gi 2...	24	260
gi 21623723 db BAC00943.1 HT-protein [Lycopersicon parvif...	24	260
gi 21623729 db BAC00945.1 HT-A protein [Lycopersicon hirs...	24	260
gi 17227037 db AA137981.1 AF442139.1 style-specific self-in...	24	260
gi 17554334 ref NP_498645.1 Muscle Positioning 4, transmem...	24	349
gi 14579227 db AA69172.1 AF289202.1 transmembrane matrix r...	24	349
gi 25395876 ref P88508 protein H14A12.6 [imported] - Caeno...	24	349
gi 15618576 ref NP_174690.1 expressed protein [Arabidopsis...	24	349
gi 15336812 ref NP_194396.1 expressed protein [Arabidopsis...	23	468
gi 17862926 db AA139940.1 SD03546P [Drosophila melanogaster]	23	628
gi 18150104 db BAB81667.1 inulin receptor [Paralichthys ...	23	628
gi 24582874 ref NP_609236.2 Cg13096-PA [Drosophila melanog...	23	628
gi 32408903 ref XP_324932.1 predicted protein [Neurospora ...	23	628

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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gi 2826739 gb AAC41350.1	chordin (Gallus gallus)	23	628	L
gi 28574692 ref NP_787974.1	CG3196-PB (Drosophila melanogaster)	23	628	L
gi 3695096 gb AAC62642.1	DN p63 gamma (Mus musculus)	22	843	L
gi 33751181 emb CAC37102.1	DN KET gamma protein (Rattus norvegicus)	22	843	L
gi 13751173 emb CAC37098.1	TA1 KET alpha protein (Rattus norvegicus)	22	843	L
gi 20428532 gb AAK8186.1	DN p73 gamma (Homo sapiens)	22	843	L
gi 1813455 gb AAK4183.1	p53	22	843	L
gi 1909383 dbj BAB87245.1	deltan p73 beta (Homo sapiens)	22	843	L
gi 7248451 gb AAK43492.1	p51 isoform delNbeta (Homo sapiens)	22	843	L
gi 20892181 ref XP_447332.1	transformation related protein...	22	843	L
gi 3695094 gb AAC62641.1	TA p63 alpha (Mus musculus)	22	843	L
gi 12060406 dbj BAB20591.1	delta N p73L (Homo sapiens)	22	843	L
gi 4801651 emb CAA72225.1	p73 splice variant (Cercopithecus)	22	843	L
gi 13751179 emb CAC37101.1	TA2 KET gamma protein (Rattus norvegicus)	22	843	L
gi 15072750 emb CAC48053.1	p63 delta (Homo sapiens)	22	843	L
gi 29470179 gb AAO74632.1	p73 (Danio rerio)	22	843	L
gi 2581764 gb AAK82420.1	p53 (Cricetus griseus)	22	843	L
gi 8217484 emb CAA92742.1	d1092A11.2 (tumor protein p73) ...	22	843	L
gi 2370178 emb CAA72221.1	second splice variant (Homo sapiens)	22	843	L
gi 21264484 sp P798201.P53	ORF1A Cellular tumor antigen p53 ...	22	843	L
gi 1188759 gb AAK87577.1	p53 tumor suppressor homolog	22	843	L
gi 1188757 gb AAK87576.1	p53 tumor suppressor homolog	22	843	L
gi 7248450 gb AAK43491.1	p51 isoform delNalpha (Homo sapiens)	22	843	L
gi 7248447 gb AAK43488.1	p51 isoform TP63beta (Homo sapiens)	22	843	L
gi 3277745 gb AAC24830.1	p53 homolog (Homo sapiens)	22	843	L
gi 473579 gb AAK41344.1	tumor suppressor p53 (Mesocricetus)	22	843	L
gi 75757178 emb CAD10682.1	p53 protein (Monodelphis domestica)	22	843	L
gi 12024746 gb AAK45609.1	TA p63 gamma (Homo sapiens)	22	843	L
gi 3695098 gb AAC62643.1	DN p63 beta (Mus musculus)	22	843	L
gi 468086 gb AAK27752.1	AF043641_1 p73 (Barbus barbus)	22	843	L
gi 6755883 ref NP_035771.1	transformation related protein ...	22	843	L
gi 1244762 gb AAK98563.1	p53 tumor suppressor homolog	22	843	L
gi 13751187 emb CAC37105.1	DN KET beta protein (Rattus norvegicus)	22	843	L
gi 13751175 emb CAC37099.1	DN KET alpha protein (Rattus norvegicus)	22	843	L
gi 23308709 ref NP_694518.1	deltanp63 isoform alpha 1; tum...	22	843	L
gi 26339452 dbj BAC33397.1	unnamed protein product (Mus musculus)	22	843	L
gi 23308711 ref NP_694519.1	deltanp63 isoform gamma; tumor...	22	843	L
gi 3695082 gb AAC62635.1	TA p63 alpha (Homo sapiens)	22	843	L
gi 16950502 gb AAC60146.1	p53 (Oryzias latipes) >gi 1208249...	22	843	L
gi 20850793 ref XP_131858.1	transformation related protein...	22	843	L
gi 13195250 gb AAK15622.1	AF314148_1 p63 DNA binding protei...	22	843	L
gi 3510328 dbj BAA35592.1	p51A (Homo sapiens) >gi 3695078 ...	22	843	L
gi 13751185 emb CAC37104.1	TA1 KET beta protein (Rattus norvegicus)	22	843	L
gi 451931 gb AAK37086.1	tumor suppressor protein (Mesocricetus)	22	843	L
gi 1813455 gb AAK4183.1	p53	22	843	L
gi 3695080 gb AAC62634.1	DN p63 gamma (Homo sapiens)	22	843	L
gi 1813455 gb AAK4183.1	p53	22	843	L
gi 13750717 emb CAF76562.1	KET protein (Homo sapiens)	22	843	L
gi 23308665 ref NP_689454.1	deltanp63 isoform alpha 2; tum...	22	843	L
gi 3445484 dbj BAA32433.1	p73H (Homo sapiens)	22	843	L
gi 76892271 gb AAK67733.1	AF253323_1 p53 tumor suppressor-1...	22	843	L
gi 17985367 gb AAK50211.1	tumor protein (Canis familiaris)	22	843	L

http://www.ncbi.nlm.nih.gov/Blast.cgi

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gi 31543818 ref NP_003713.3	tumor protein p73-like; tumor ...	22	843	L
gi 19909991 dbj BAB87244.1	deltan p73 alpha (Homo sapiens)...	22	843	L
gi 4101545 gb AAK01196.1	tumor suppressor protein p53 (Ory...	22	843	L
gi 1813455 gb AAK4183.1	p53	22	843	L
gi 1244762 gb AAK98564.1	p53 tumor suppressor homolog	22	843	L
gi 7440008 dbj JG6176	tumor suppressor protein p53 - Chine...	22	843	L
gi 12856636 dbj BAB30732.1	unnamed protein product (Mus mu...	22	843	L
gi 19850152 gb AAK9584.1	AF285104_1 p53-like transcription...	22	843	L
gi 1720915 emb CAA81954.1	p73 delta-N protein (Mus musculus)	22	843	L
gi 1193701 sp Q00366.P53	MESDV Cellular tumor antigen p53 (r...	22	843	L
gi 7689273 gb AAK67734.1	AF253324_1 p73-like protein (Mya a...	22	843	L
gi 3695088 gb AAC62638.1	DN p63 beta (Homo sapiens) >gi 12...	22	843	L
gi 12370177 emb CAA72219.1	first splice variant (Homo sapiens)	22	843	L
gi 1310310 dbj BAA32593.1	p51B (Homo sapiens) >gi 7248446 ...	22	843	L
gi 1890327 emb CAA70109.1	p53 tumour suppressor (Cricetulu...	22	843	L
gi 1748452 gb AAK43493.1	p51 isoform delNdelta (Homo sapiens)	22	843	L
gi 12060407 dbj BAB20631.1	DN p63 alpha (Gallus gallus)	22	843	L
gi 3695092 gb AAC62640.1	TA p63 beta (Mus musculus)	22	843	L
gi 10720154 sp Q977A1.P53	TP63 Cellular tumor antigen p53 ...	22	843	L
gi 1748448 gb AAK43489.1	p51 isoform TP63delta (Homo sapi...	22	843	L
gi 3695090 gb AAC62639.1	TA p63 gamma (Mus musculus)	22	843	L
gi 12994281 sp Q09185.P53	CRIGR Cellular tumor antigen p53 (...)	22	843	L
gi 12643523 sp Q95XK1.P73	CERKX tumor protein p73 (p53-like...	22	843	L
gi 4885645 ref NP_005418.1	tumor protein p73; p53-related ...	22	843	L

Alignments

gi 31207283 ref XP_312608.1	ENSANGP00000014785 (Anopheles gambiae)	22	843	L
gi 21295912 gb EAA07957.1	ENSANGP00000014785 (Anopheles gambiae str. PESST)	22	843	L

Length = 338
Score = 33.7 bits (72), Expect = 0.30
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 1 KICSCPRD 9
KICSCPRD
Subject: 309 KICSCPRD 317

gi 21355617 ref NP_651115.1	CG10873-PA (Drosophila melanogaster)	22	843	L
gi 1211767 gb AAK40428.1	AF224713_1 transcription factor p53 (Drosophila melano)	22	843	L
gi 1211769 gb AAK40428.1	AF224714_1 transcription factor p53 (Drosophila melano)	22	843	L
gi 17381624 gb AAK61572.1	AF244918_1 p53 tumor suppressor-like protein (Drosophi)	22	843	L
gi 8272608 gb AAK74277.1	AF250918_1 transcription factor (Drosophila melanogast	22	843	L
gi 8453116 gb AAK75270.1	AF263722_1 transcription factor p53 (Drosophila melano	22	843	L
gi 10726710 gb AAK56087.2	CG10873-PA (Drosophila melanogaster)	22	843	L
gi 17861328 gb AAK39241.1	GH11591P (Drosophila melanogaster)	22	843	L

http://www.ncbi.nlm.nih.gov/Blast.cgi

7/10/2003

gi|18032162|gb|AA156639.1|AF192555.1 p53-like regulator of apoptosis and cell cyc
melanogaster]
Length = 385

Score = 31.2 bits (66), Expect = 1.8
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 1 KICSCPKRD 9
KIC+CPKRD
Sbjct: 259 KICTCPKRD 267

>gi|25009887|gb|AA171112.1| AT28346p [Drosophila melanogaster]
Length = 519

Score = 31.2 bits (66), Expect = 1.8
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 1 KICSCPKRD 9
KIC+CPKRD
Sbjct: 393 KICTCPKRD 401

>gi|1673504|emb|CA66181.1| G protein-coupled receptor kinase GRK4B [Rattus no
Length = 544

Score = 26.1 bits (54), Expect = 60
Identities = 8/12 (66%), Positives = 9/12 (75%), Gaps = 3/12 (25%)

Query: 1 KICSC---PKRD 9
KICSC PKR+
Sbjct: 508 KICSCILRPKN 519

>gi|12621084|ref|NP_075217.1| G protein-coupled receptor kinase 2, groucho ger
norvegicus]
Length = 575

Score = 26.1 bits (54), Expect = 60
Identities = 8/12 (66%), Positives = 9/12 (75%), Gaps = 3/12 (25%)

Query: 1 KICSC---PKRD 9
KICSC PKR+
Sbjct: 539 KICSCILRPKN 550

>gi|23867780|db|BAC21014.1| claudin4L2 [Xenopus laevis]
Length = 213

Score = 24.8 bits (51), Expect = 144
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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CSCPKR+
Sbjct: 183 CSCPKRE 189

>gi|21623719|db|BAC00941.1| HT-protein [Lycopersicon peruvianum]
Length = 96

Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9
CSCPK+D
Sbjct: 61 CSCPKRD 67

>gi|17227039|gb|AA137982.1|AF442140.1 scyle-specific self-incompatibility putat;
HT-A2 [Solanum chacoense]
Length = 77

Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9
CSCPK+D
Sbjct: 44 CSCPKRD 50

>gi|21623726|db|BAC00944.1| HT-A protein [Lycopersicon chmielewskii]
Length = 89

Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9
CSCPK+D
Sbjct: 55 CSCPKRD 61

>gi|23113187|ref|ZP_00098587.1| hypothetical protein [Desulfitobacterium hafnien
Length = 590

Score = 24.0 bits (49), Expect = 260
Identities = 7/9 (77%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query: 2 ICS-CPKRD 9
IC+CPKRD
Sbjct: 78 ICNCPKRD 86

>gi|30039744|ref|NP_835472.1| rolling circle replication protein [Vibrio cholera
gi|29888081|gb|AA093096.1| rolling circle replication protein [Vibrio cholerae ph
Length = 359

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 ICSCPK 7
ICSCPK
Sbjct: 80 ICSCPK 85

>gi|2955659|ref|NP_817241.1| ORP82 [Pinus koraiensis]
gi|29469758|gb|AA074086.1| ORP82 [Pinus koraiensis]
Length = 82

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 1 KICSCP 6
KICSCP
Sbjct: 19 KICSCP 24

>gi|21623723|db|BAC00943.1| HT-protein [Lycopersicon parviflorum]
Length = 90

Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9
CSCPKRD
Sbjct: 55 CSCPKRD 61

>gi|21623729|db|BAC00945.1| HT-A protein [Lycopersicon hirsutum]
Length = 84

Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9
CSCPKRD
Sbjct: 50 CSCPKRD 56

>gi|17227037|gb|AAU37981.1|AF442139.1 style-specific self-incompatibility putative
HT-A1 [Solanum chacoense]
Length = 99

Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPKRD 9
CSCPKRD
Sbjct: 66 CSCPKRD 72

<http://www.ncbi.nlm.nih.gov/blast.cgi>

7/10/2003

>gi|17554334|ref|NP_498645.1| Muscle Positioning 4, transmembrane matrix receptor
embryonic muscle attachment and epithelial cell adhesion
at hemidesmosomes (230.1 kD) (mup-4) [Caenorhabditis elegans]
gi|15789306|gb|AA28092.5| Muscle positioning protein 4 [Caenorhabditis elegans]
Length = 2104

Score = 23.5 bits (48), Expect = 349
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 KICSCP 7
KIC CPK
Sbjct: 1476 KICGCPK 1482

>gi|14579227|gb|AAK69172.1|AF289202.1 transmembrane matrix receptor MUP-4 [Caenorhabditis elegans]
Length = 2104

Score = 23.5 bits (48), Expect = 349
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 KICSCP 7
KIC CPK
Sbjct: 1476 KICGCPK 1482

>gi|25395876|db|P88508 protein H14A12.6 (imported) - Caenorhabditis elegans
Length = 794

Score = 23.5 bits (48), Expect = 349
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 KICSCP 7
KIC CPK
Sbjct: 144 KICGCPK 150

>gi|15218576|ref|NP_174690.1| expressed protein [Arabidopsis thaliana]
gi|25518170|db|B86467 hypothetical protein F23M19.5 - Arabidopsis thaliana
gi|5091617|gb|AAD39605.1|AC007454.4 Contains similarity to gi|479356 protein kinase
is a member of the PF10054 S-locus glycoprotein family
and contains a PF10069 Eukaryotic protein kinase
domain. [Arabidopsis thaliana]
gi|19699084|gb|AAU90909.1| At1g34300/F23M19.5 [Arabidopsis thaliana]
gi|24111429|gb|AAU46865.1| At1g34300/F23M19.5 [Arabidopsis thaliana]
Length = 829

Score = 23.5 bits (48), Expect = 349
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9
ICSCP R+
Sbjct: 288 ICSCPSRN 295

<http://www.ncbi.nlm.nih.gov/blast.cgi>

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>gi|15236812|ref|NP_194396.1| expressed protein [Arabidopsis thaliana]
 gi|7487040|db|TT08932| hypothetical protein T15N24.110 - Arabidopsis thaliana
 gi|4938504|emb|CA843862.1| putative protein [Arabidopsis thaliana]
 gi|17269518|emb|CA879521.1| putative protein [Arabidopsis thaliana]
 Length = 806

Score = 23.1 bits (47), Expect = 468
 Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 4 SCPRND 9

Subject: 184 SCPRND 189

>gi|17862926|gb|AAJ3940.1| SD03546p [Drosophila melanogaster]
 Length = 681

Score = 22.7 bits (46), Expect = 628
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 KICSCPKR 8

KI SCPKR

Subject: 311 KIPSCPKR 318

>gi|18150104|db|BA83667.1| insulin receptor [Paralichthys olivaceus]
 Length = 1369

Score = 22.7 bits (46), Expect = 628
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 1 KICSCPKR 9

K+C+CPK D

Subject: 705 KVCACPKRD 713

>gi|24582874|ref|NP_609235.2| CG13096-PA [Drosophila melanogaster]
 gi|17297428|gb|AAF52687.1| CG13096-PA [Drosophila melanogaster]
 Length = 681

Score = 22.7 bits (46), Expect = 628
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 KICSCPKR 8

KI SCPKR

Subject: 311 KIPSCPKR 318

>gi|32408903|ref|XP_324932.1| predicted protein [Neurospora crassa]
 gi|28925918|gb|FA34913.1| predicted protein [Neurospora crassa]
 Length = 229

Score = 22.7 bits (46), Expect = 628
 Identities = 6/7 (85%), Positives = 6/7 (85%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 2 ICSCPKR 8
 ICSCP R
 Subject: 134 ICSCPKR 140

>gi|2826739|gb|AAC4250.1| chordin [Gallus gallus]
 Length = 940

Score = 22.7 bits (46), Expect = 628
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 ICSCPKR 8

ICSC KR

Subject: 716 ICSCPKR 722

>gi|28574699|ref|NP_787974.1| CG33196-PB [Drosophila melanogaster]
 gi|28380266|gb|AAJ0358.2|AE003576.45 CG33196-PB [Drosophila melanogaster]
 Length = 23054

Score = 22.7 bits (46), Expect = 628
 Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 2 ICSCPKR 8

ICSCP+R

Subject: 21341 ICSCPKR 21347

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICSCP 6

ICSCP

Subject: 20821 ICSCP 20825

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICSCP 6

ICSCP

Subject: 17656 ICSCP 17660

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICSCP 6

ICSCP

Subject: 16586 ICSCP 16590

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICSCP 6
 ICSCP 6
 Sbjct: 12381 ICSCP 12385

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICSCP 6
 ICSCP 6
 Sbjct: 10780 ICSCP 10784

Score = 21.0 bits (42), Expect = 2037
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 ICSCP 6
 ICSCP 6
 Sbjct: 9815 ICSCP 9819

Score = 18.5 bits (36), Expect = 11887
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 ICSCP 6
 +CSCP
 Sbjct: 21018 VCSCP 21022

Score = 18.5 bits (36), Expect = 11887
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 ICSCP 6
 +CSCP
 Sbjct: 20927 VCSCP 20931

Score = 18.5 bits (36), Expect = 11887
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 ICSCP 6
 IC+CP
 Sbjct: 11743 ICTCP 11747

Score = 18.5 bits (36), Expect = 11887
 Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 2 ICSCP 7
 IC CRK
 Sbjct: 8799 ICTCPK 8804

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

Score = 18.5 bits (36), Expect = 11887
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 ICSCP 6
 IC+CP
 Sbjct: 3933 ICTCP 3937

Score = 18.5 bits (36), Expect = 11887
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 ICSCP 6
 IC+CP
 Sbjct: 2479 ICTCP 2483

Score = 18.5 bits (36), Expect = 11887
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 ICSCP 6
 +CSCP
 Sbjct: 1979 VCSCP 1983

[>gi|13695096|gb|AAC62642.1|] **[L]** DN p63 gamma [Mus musculus]
 Length = 389

Score = 22.3 bits (45), Expect = 843
 Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9
 IC+CP RD
 Sbjct: 250 ICACPRD 257

[>gi|13751181|emb|CAC37102.1|] **[L]** DN KER gamma protein [Rattus norvegicus]
 Length = 393

Score = 22.3 bits (45), Expect = 843
 Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPGRD 9
 IC+CP RD
 Sbjct: 250 ICACPRD 257

[>gi|13751173|emb|CAC37098.1|] **[L]** TAI KER alpha protein [Rattus norvegicus]
 Length = 663

Score = 22.3 bits (45), Expect = 843
 Identities = 6/8 (75%), Positives = 7/8 (87%)

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

Query: 2 ICSCPKRD 9
IC+CP RD
Sbjct: 327 ICACPKRD 334

>gi|20428532|gb|AAK81886.1| DN p73 gamma [Homo sapiens]
Length = 426

Score = 22.3 bits (45), Expect = 843
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9
IC+CP RD
Sbjct: 245 ICACPKRD 252

>gi|1813455|gb|AA841833.1| P53
Length = 238

Score = 22.3 bits (45), Expect = 843
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9
IC+CP RD
Sbjct: 167 ICACPKRD 174

>gi|19909983|dbj|BAB87245.1| DN p73 beta [Homo sapiens]
gi|20428530|gb|AAK81885.1| DN p73 beta [Homo sapiens]
Length = 450

Score = 22.3 bits (45), Expect = 843
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9
IC+CP RD
Sbjct: 245 ICACPKRD 252

>gi|7248451|gb|AAK43492.1| p51 isoform delnbeta [Homo sapiens]
Length = 461

Score = 22.3 bits (45), Expect = 843
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9
IC+CP RD
Sbjct: 250 ICACPKRD 257

>gi|20892181|ref|XP_147232.1| transformation related protein 63 [Mus musculus]
Length = 465

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 22.3 bits (45), Expect = 843
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9
IC+CP RD
Sbjct: 129 ICACPKRD 136

>gi|3695094|gb|AA62641.1| TAP63 alpha [Mus musculus]
Length = 680

Score = 22.3 bits (45), Expect = 843
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9
IC+CP RD
Sbjct: 344 ICACPKRD 351

>gi|12060406|dbj|BAB20591.1| delta N p73L [Homo sapiens]
Length = 501

Score = 22.3 bits (45), Expect = 843
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9
IC+CP RD
Sbjct: 165 ICACPKRD 172

>gi|4803651|emb|CAA72225.1| p73 splice variant [Cercopithecus aethiops]
Length = 499

Score = 22.3 bits (45), Expect = 843
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9
IC+CP RD
Sbjct: 294 ICACPKRD 301

>gi|11751179|emb|CAC37101.1| TAP2 KET gamma protein [Rattus norvegicus]
Length = 487

Score = 22.3 bits (45), Expect = 843
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPKRD 9
IC+CP RD
Sbjct: 344 ICACPKRD 351

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

>gi|15072750|emb|CAC48053.1| p63 delta [Homo sapiens]

Length = 232

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPRD 9

IC+CP RD

Sbjct: 192 ICACPRD 199

>gi|29470179|gb|AA074632.1| p73 [Danio rerio]

Length = 640

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPRD 9

IC+CP RD

Sbjct: 301 ICACPRD 308

>gi|2581764|gb|AA82420.1| p53 [Cricketus griseus]

Length = 205

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPRD 9

IC+CP RD

Sbjct: 149 ICACPRD 156

>gi|8217484|emb|CA892742.1| dU1092A11.2 (tumor protein p73) [Homo sapiens]

Length = 661

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPRD 9

IC+CP RD

Sbjct: 319 ICACPRD 326

>gi|2370178|emb|CAA72221.1| second splice variant [Homo sapiens]

Length = 588

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPRD 9

IC+CP RD

Sbjct: 246 ICACPRD 253

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

>gi|21264484|emb|P79820|p53 ORYL4 Cellular tumor antigen p53 (tumor suppressor p; gi|4101544|gb|AAD01195.1| tumor suppressor protein p53 [oryzias latipes])

Length = 352

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPRD 9

IC+CP RD

Sbjct: 255 ICACPRD 262

>gi|1184759|gb|AA87577.1| p53 tumor suppressor homolog

Length = 189

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPRD 9

IC+CP RD

Sbjct: 90 ICACPRD 97

>gi|1184757|gb|AA87576.1| p53 tumor suppressor homolog

Length = 228

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPRD 9

IC+CP RD

Sbjct: 98 ICACPRD 105

>gi|7248450|gb|AA43491.1| p51 isoform delNalpha [Homo sapiens]

Length = 386

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPRD 9

IC+CP RD

Sbjct: 250 ICACPRD 257

>gi|7248447|gb|AA43488.1| p51 isoform TAp63beta [Homo sapiens]

Length = 516

Score = 22.3 bits (45), Expect = 843

Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPRD 9

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

IC+CP RD
Sbjct: 305 ICACPRGD 312

>gi|3273745|gb|AAC24830.1| p53 homolog [Homo sapiens]
Length = 356

Score = 22.3 bits (45), Expect = 843
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPRKD 9

IC+CP RD
Sbjct: 250 ICACPRGD 257

>gi|473579|db|AA041344.1| tumor suppressor p53 [Mesocricetus auratus]
Length = 396

Score = 22.3 bits (45), Expect = 843
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 ICSCPRKD 9

IC+CP RD
Sbjct: 277 ICACPRGD 284

Get selected sequences Select all Deselect all

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PP

Posted date: Jul 10, 2003 1:49 AM

Number of letters in database: 474,244,320

Number of sequences in database: 1,477,204

Lambda K H
0.358 0.291 2.08

Gapped

Lambda K H
0.294 0.110 0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Hits to DB: 8,062,146

Number of Sequences: 1477204

Number of extensions: 39018

Number of successful extensions: 1058

Number of sequences better than 20000.0: 100

Number of HSP's better than 20000.0 without gapping: 1001

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1058

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

length of query: 9
length of database: 474,244,320
effective HSP length: 0
effective length of query: 9
effective length of database: 474,244,320
effective search space: 4268198880
effective search space used: 4268198880
T: 11
A: 40
X1: 14 (7.2 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 35 (19.9 bits)
S2: 35 (18.0 bits)

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

EXHIBIT H

NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057861590-0767-27408

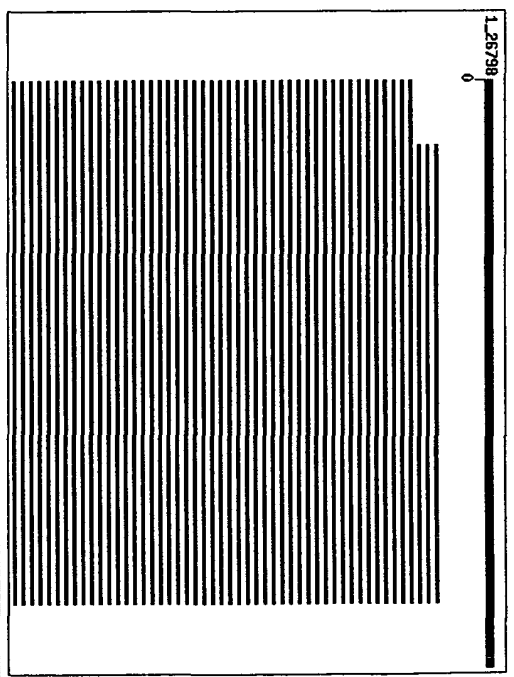
Query= SEQID25
(9 letters)

Database: All non-redundant Genbank CDS
translations+PDB+SwissProt+PIR+PRF
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQ
Taxonomy reports

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Related Structures

Sequences producing significant alignments:

	Score	E
Sequences producing significant alignments:	(bits)	Value
gi 31207283 ref XP_312608.1 ENSANGP00000014785 (Anopheles ...	2.8	14
gi 21355617 ref NP_651115.1 CG10873-PA (Drosophila melanog...	2.6	80
gi 25009887 gb AA071112.1 AN28346p (Drosophila melanogaster)	2.6	80
gi 129372 sp P10361 P53_FAT Cellular tumor antigen p53 (Tum...	2.5	108
gi 7259331 db BA02786.1 p53 (Macaca fuscata)	2.5	108
gi 693787 gb AA31269.1 tumor suppressor (Canis familiaris)	2.5	108
gi 8400738 ref NP_000537.2 tumor protein p53 (Homo sapiens...	2.5	108
gi 4950581 gb AA034216.1 AF07574.1 tumor suppressor protei...	2.5	108
gi 1709531 sp P51664 P53_SHEEP Cellular tumor antigen p53 (...	2.5	108
gi 129369 sp P04637 P53_HUMAN Cellular tumor antigen p53 (T...	2.5	108
gi 1836145 gb AA046899.1 sequence-specific transcription f...	2.5	108
gi 11321107 gb AA034052.1 p53 tumor suppressor (Rattus nor...	2.5	108
gi 1626760 db BA06969.1 p53 (Meriones unguiculatus)	2.5	108
gi 21730310 pdb 1GZH C Chain C, Crystal Structure Of The Br...	2.5	108
gi 6755881 ref NP_035770.1 transformation related protein ...	2.5	108
gi 200201 gb AA39882.1 p53	2.5	108
gi 1154648 emb CA062905.1 p53 (Equus caballus)	2.5	108
gi 2811079 sp O12946 P53_PLAWE Cellular tumor antigen p53 (...	2.5	108
gi 1171969 sp P41685 P53_FETCA Cellular tumor antigen p53 (...	2.5	108
gi 1000577 gb AA042022.1 p53 (Canis familiaris)	2.5	108
gi 975651 emb CA062450.1 p53 (Callionymus lyra)	2.5	108
gi 20900490 ref XP_128695.1 similar to transformation rela...	2.5	108
gi 8698976 db AA078535.1 AF223795.1 tumor suppressor p53 (On...	2.5	108

g1.1729491[idb]	hAA08629.1	p53 gene product [Bos primigenius]	25	108	L
g1.4711632[idb]	hAD28535.1	hA15121.1 tumor suppressor protei...	25	108	L
g1.10720196[idb]	hO96W678.P53	BARBU Cellular tumor antigen p53 ...	25	108	L
g1.1223827[prf]	l1001197A	antigen p53, tumor	25	108	L
g1.11342599[emb]	hCAC1747.1	transformation related protein ...	25	108	L
g1.18659503[ref]	h571402.1	tumor protein p53; tumor suppr...	25	108	L
g1.10720186[idb]	hQ70B21.P53	PIG Cellular tumor antigen p53 (T...	25	108	L
g1.2829194[idb]	hAC26190.1	tumor suppressor ortholog [Xiphop...	25	108	L
g1.4966230[idb]	hAA78379.1	p53 [Canis familiaris]	25	108	L
g1.13591878[ref]	hF1NP_112251.1	tumor protein p53; tumor prote...	25	108	L
g1.1239374[idb]	hF017193	p53-XENLA Cellular tumor antigen p53 (T...	25	108	L
g1.53317461[idb]	hAD42225.1	p53 protein [Canis familiaris]	25	108	L
g1.1389187[idb]	hAB18935.1	tumor-suppressor [Equus caballus]	25	108	L
g1.2961247[idb]	hAAC05704.1	tumor suppressor p53 [Mus musculus]	25	108	L
g1.13575072[idb]	hAAK94783.1	transformation related protein 5...	25	108	L
g1.8658921[idb]	hAF78533.1	hAF223793.1 tumor suppressor p53 [On...	25	108	L
g1.28975327[idb]	hAA060156.1	tumor suppressor p53; p53aa [Mue...	25	108	L
g1.42595056[idb]	hAD34245.1	hAF01573.1 tumor suppressor protei...	25	108	L
g1.6841071[idb]	hAA78891.1	hAF142298.1 p53 protein [Sus scrofa]	25	108	L
g1.535721[emb]	hCA25323.1	p53 [Mus musculus]	25	108	L
g1.13897097[idb]	hAA683290.1	hAF475081.1 p53 [Dolipnapterus le...	25	108	L
g1.14039918[idb]	hAAK53397.1	hAF367373.1 p53 tumor suppressor (...)	25	108	L
g1.28849929[ref]	hF1NP_776626.1	p53 tumor suppressor phosphopr...	25	108	L
g1.3024331[idb]	hP56423	p53_MNCFR Cellular tumor antigen p53 (...)	25	108	L
g1.2781308[idb]	hYCSA	Chain A, p53-33bp2 Complex	25	108	S
g1.642241[emb]	hCA25652.1	p53 (Homo sapiens)	25	108	L
g1.10720196[idb]	hO96W79.P53	TETNU Cellular tumor antigen p53 ...	25	108	L
g1.10720197[idb]	hO9WUR6.P53	CAVPO Cellular tumor antigen p53 ...	25	108	L
g1.5064491[emb]	hCA4623.1	p53 transformation suppressor [Ho...	25	108	L
g1.1293366[idb]	hA31060.P53	CHICK Cellular tumor antigen p53 (T...	25	108	L
g1.1619833[idb]	hAB15961.1	p53 [Canis familiaris]	25	108	L
g1.14719450[idb]	hH081A	Chain A, Crystal Structure of The Mo...	25	108	S
g1.506445[emb]	hCA46231.1	p53 transformation suppressor [Ho...	25	108	L
g1.50817831[idb]	hA39531.1	hAF151353.1 tumor suppressor p53 [M...	25	108	L
g1.10720190[idb]	hO36006.P53	ARVIO Cellular tumor antigen p53 ...	25	108	L
g1.12233851[idb]	hAA92052.1	p53 [Xiphophorus maculatus]	25	108	L
g1.5064443[emb]	hCA42630.1	p53 transformation suppressor [Ho...	25	108	L
g1.21730308[idb]	hGZHA	Chain A, Crystal Structure of The Br...	25	108	S
g1.339814[idb]	hAA61211.1	p53 antigen	25	108	L
g1.2842741[idb]	hO953310.P53	RABIT Cellular tumor antigen p53 (...)	25	108	L
g1.17530891[idb]	hAB39322.1	cellular phosphoprotein p53	25	108	L
g1.339816[idb]	hAA61212.1	p53 antigen	25	108	L
g1.10720193[idb]	hO92143.P53	XTRMA Cellular tumor antigen p53 ...	25	108	L
g1.5064441[emb]	hCA46232.1	p53 transformation suppressor [Ho...	25	108	L
g1.150363691[idb]	hO295371.P53	CANFA Cellular tumor antigen p53 (...)	25	108	L
g1.10720192[idb]	hO933791.P53	ICMPU Cellular tumor antigen p53 ...	25	108	L
g1.1463021[idb]	hAC07335.1	p53 [Canis familiaris]	25	108	L
g1.4815331[idb]	hS38824	cellular tumor antigen p53, minor sp1...	25	108	L
g1.386994[idb]	hAA5987.1	phosphoprotein p53 (Homo sapiens)	25	108	L
g1.545102[idb]	hAC60746.1	p53 [Xenopus laevis]	25	108	L
g1.10720191[idb]	hO575361.P53	XTRPE Cellular tumor antigen p53 ...	25	108	L

q11.20151154 p[db]1KXZY4 Chain A, Crystal Structure of The 53...	25	108	S
q11.3024332 p[db]1P56424 P53_MAMCUT Cellular tumor antigen p53 (...)	25	108	S
q11.1310770 p[db]1ITR54 Chain A, P53 Core Domain in Complex W...	25	108	L
q11.12938365 p[db]1AAB80959.1 mutant p53 [nactua norvegicus]	25	108	L
q11.5064393 emb CAA42628.1 p53 transformation suppressor [Ho...	25	108	L
q11.129367 p[db]1P13481 P53_CERAB Cellular tumor antigen p53 (T...	25	108	L
q11.1503451 emb CAA42634.1 p53 transformation suppressor [Ho...	25	108	L
q11.120371 p[db]1P02340 P53_MOUSE Cellular tumor antigen p53 (T...	25	108	L
q11.129373 p[db]1P25035 P53_ONCMY Cellular tumor antigen p53 (T...	25	108	L
q11.465814 emb CAA46572.1 p53 [Xenopus laevis]	25	108	L
q11.29468129 p[db]1A085406.1 A2F5873.1 tumor suppressor p53 [...]	25	108	L
q11.4959054 p[db]1A0D34214.1 A071572.1 tumor suppressor protei...	25	108	L
q11.263448179 p[db]1BAC371729.1 unnamed protein product [Mus mu...	25	108	L
q11.5755284 p[db]1BAA03927.1 p53 protein [Felis catus]	25	108	L
q11.24545420 p[db]1AAB72099.1 chimeric tumor suppressor [synth...	25	108	L
q11.28333362 sp Q29480 P53_EGQUS Cellular tumor antigen p53 (...)	25	108	L
q11.2896679 p[db]1P789821 sp P789821 P53_HORSE Cellular tumor antigen p53 (...)	25	108	L
q11.2842672 sp Q64662 P53_SPEBE Cellular tumor antigen p53 (...)	25	108	L
q11.5064393 emb CAA42628.1 p53 transformation suppressor [Ho...	25	108	L
q11.236867780 p[db]1BAC21014.1 claudin412 [Xenopus laevis]	25	144	L
q11.18150106 p[db]1BAC83668.1 insulin receptor [Paralichthys ...]	24	194	L
q11.16250119 p[db]1BAC00941.1 HM-protein [Lycopersicon peruv...	24	260	L
q11.172227039 p[db]1AAB57982.1 A442140.1 style-specific self-in...	24	260	L
q11.21633723 p[db]1BAC00944.1 HM-A protein [Lycopersicon chmi...	24	260	L
q11.21633723 p[db]1BAC00943.1 HM-protein [Lycopersicon parvif...	24	260	L

Alignement

Get selected sequences

Select all

Deselect all

[>qi|31207283|ref|XP_312608.1| ENSANGP00000014785 (Anopheles gambiae)
 qi|21595812|gb|EAA07957.1| ENSANGP00000014785 (Anopheles gambiae str. PEST)
 Length = 338

Score = 28.2 bits (59), Expect = 14
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 2 VCSCPKRD 5

Subject: 310 ICSCP/KRD 317

1 >gi21235561.ref|NP_651115.1 1 CG10873-PA (Drosophila melanogaster)
 1 gi17211671.gb|AAAF60427.1 1 AF224713.1 1 transcription factor p53 (Drosophila melano
 1 gi17211691.gb|AAAF60428.1 1 AF224714.1 1 transcription factor p53 (Drosophila melano
 1 gi17381624.gb|AAAF61572.1 1 AF224918.1 1 p53 tumor suppressor-like protein (Drosophi
 1 gi18272608.gb|AAAF4227.1 1 AF250918.1 1 transcription factor (Drosophila melanogaster)
 1 gi18453176.gb|AAAF5270.1 1 AF263722.1 1 transcription factor p53 (Drosophila melano
 1 gi10726710.gb|AAAF56087.2 1 CG10873-PA (Drosophila melanogaster)

gi|17861528|gb|AA138241.1| **1** GH11591p [Drosophila melanogaster]
 gi|18032162|gb|AA156539.1|AF192555.1 p53-like regulator of apoptosis and cell cyc
 melanogaster]
 Length = 385

Score = 25.7 bits (53), Expect = 80
 Identities = 6/8 (75%), Positives = 8/8 (100%)

Query: 2 VCSCEPRD 9
 +C+CEPRD
 Sbjct: 260 ICTCEPRD 267

gi|2509887|gb|AA171112.1| AT28346p [Drosophila melanogaster]
 Length = 519

Score = 25.7 bits (53), Expect = 80
 Identities = 6/8 (75%), Positives = 8/8 (100%)

Query: 2 VCSCEPRD 9
 +C+CEPRD
 Sbjct: 394 ICTCEPRD 401

gi|129312|gb|P10361|P53_RAT Cellular tumor antigen p53 (Tumor suppressor p53)
 gi|92070|pir|S02192 cellular tumor antigen p53 - rat
 gi|56829|emb|CA31457.1| **1** nuclear protein p53 (AA 1 - 391) [Rattus norvegicus]
 Length = 391

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
 RVC+CP RD
 Sbjct: 271 RVCACPRD 279

gi|7259331|db|BA92786.1| p53 [Macaca fuscata]
 Length = 181

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
 RVC+CP RD
 Sbjct: 148 RVCACPRD 156

gi|693787|db|AA31269.1| tumour suppressor [Canis familiaris]
 Length = 32
 Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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Query: 1 RVCSCPRD 9
 RVC+CP RD
 Sbjct: 4 RVCACPRD 12

gi|18400738|ref|NP_000537.2| **1** tumor protein p53 [Homo sapiens]
 gi|525300|pir|IDNHU53 cellular tumor antigen p53 [validated] - human
 gi|35214|emb|CA38095.1| **1** protein p53 [Homo sapiens]
 gi|506437|emb|CA42627.1| **1** p53 transformation suppressor [Homo sapiens]
 gi|3041867|gb|AA12971.1| **1** p53 [Homo sapiens]
 gi|4732147|gb|AA28628.1|AF136271.1 **1** tumor suppressor protein p53 [Homo sapiens]
 gi|11066970|gb|AA628785.1|AF307851.1 **1** p53 protein [Homo sapiens]
 Length = 393

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
 RVC+CP RD
 Sbjct: 273 RVCACPRD 281

gi|4959058|gb|AA34216.1|AF071574.1 tumor suppressor protein p53 [Oncomyoblastus]
 Length = 265

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
 RVC+CP RD
 Sbjct: 252 RVCACPRD 260

gi|1709531|gb|P51664|P53_SHEEP Cellular tumor antigen p53 (Tumor suppressor p53)
 gi|602357|emb|CA57345.1| p53 [Ovis aries]
 Length = 382

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
 RVC+CP RD
 Sbjct: 262 RVCACPRD 270

gi|129312|gb|P10361|P53_HUMAN **1** Cellular tumor antigen p53 (Tumor suppressor p53)
 p53) (Antigen NY-CO-13)
 gi|35210|emb|CA26306.1| **1** p53 tumor antigen (aa 1-7) [Homo sapiens]
 gi|189476|gb|AA59988.1| **1** phosphoprotein p53
 gi|7595312|gb|AA64408.1|AF192534.1 tumor suppressor protein p53 [Expression vect
 Length = 393

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9

RVC+CP RD

Subject: 273 RVCACPKRD 281

>gi|1836145|gb|AA046899.1| sequence-specific transcription factor [Equidae]
 Length = 263

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9

RVC+CP RD

Subject: 224 RVCACPKRD 232

>gi|11321107|gb|AA034052.1| p53 tumor suppressor [Rattus norvegicus]
 Length = 53

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9

RVC+CP RD

Subject: 12 RVCACPKRD 20

>gi|1626760|db|BA06969.1| p53 [Meriones unguiculatus]
 Length = 390

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9

RVC+CP RD

Subject: 271 RVCACPKRD 279

>gi|21730310|pdb|1GZH|C 5 Chain C, Crystal Structure Of The Brct Domains Of Hum
 To The p53 Tumor Suppressor
 Length = 198

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9

RVC+CP RD

Subject: 179 RVCACPKRD 187

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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>gi|6755881|ref|NP_035770.1| 5 transformation related protein 53 [Mus musculus]
 gi|53576|emb|CA025625.1| 5 p53 polypeptide (aa 1-390) [Mus musculus]
 gi|871421|emb|CA025420.1| 5 cellular tumor antigen p53 [Mus musculus]
 Length = 390

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9

RVC+CP RD

Subject: 270 RVCACPKRD 278

>gi|200201|gb|AA039882.1| 5 p53
 Length = 390

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9

RVC+CP RD

Subject: 270 RVCACPKRD 278

>gi|1154648|emb|CA062805.1| p53 [Equus caballus]
 Length = 196

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9

RVC+CP RD

Subject: 140 RVCACPKRD 148

>gi|2811079|sp|O12946|P53_PLAFB Cellular tumor antigen p53 (Tumor suppressor p53;
 gi|1922902|emb|CA070223.1| p53 [Platichthys flesus]
 Length = 366

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9

RVC+CP RD

Subject: 248 RVCACPKRD 256

>gi|1171969|sp|P41685|P53_FELCA Cellular tumor antigen p53 (Tumor suppressor p53;
 gi|538225|db|BA05653.1| p53 [Felis catus]
 Length = 386

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 1 RVCSCPRD 9
RVC-CP RD
Sbjct: 266 RVCACPRD 274

>gi|1000577|gb|AA042022.1| p53 [Canis familiaris]
Length = 276

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
RVC-CP RD
Sbjct: 237 RVCACPRD 245

>gi|975651|emb|CA62450.1| p53 [Callionymus lyra]
Length = 45

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
RVC-CP RD
Sbjct: 37 RVCACPRD 45

>gi|20900430|ref|XP_128695.1| similar to transformation related protein 53 [H
Length = 151

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
RVC-CP RD
Sbjct: 114 RVCACPRD 122

>gi|8698976|gb|AA078535.1|AF223795.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8698978|gb|AA078536.1|AF223796.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8698980|gb|AA078537.1|AF223797.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8698982|gb|AA078538.1|AF223798.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8698984|gb|AA078539.1|AF223799.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8698986|gb|AA078540.1|AF223800.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8698988|gb|AA078541.1|AF223801.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8698990|gb|AA078542.1|AF223802.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8698992|gb|AA078543.1|AF223803.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8698994|gb|AA078544.1|AF223804.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8698996|gb|AA078545.1|AF223805.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8698998|gb|AA078546.1|AF223806.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8699000|gb|AA078547.1|AF223807.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8699002|gb|AA078548.1|AF223808.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8699004|gb|AA078549.1|AF223809.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8699006|gb|AA078550.1|AF223810.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8699008|gb|AA078551.1|AF223811.1 tumor suppressor p53 [Oncomyrmecus tahaytscha

http://www.ncbi.nlm.nih.gov/Blast.cgi

7/10/2003

gi|8699010|gb|AA078552.1|AF223812.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8699012|gb|AA078553.1|AF223813.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8699014|gb|AA078554.1|AF223814.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8699016|gb|AA078555.1|AF223815.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8699018|gb|AA078556.1|AF223816.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8699020|gb|AA078557.1|AF223817.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
gi|8699022|gb|AA078558.1|AF223818.1 tumor suppressor p53 [Oncomyrmecus tahaytscha
Length = 146

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
RVC-CP RD
Sbjct: 42 RVCACPRD 50

>gi|1729419|dbj|BA008629.1| p53 gene product [Bos primigenius]
Length = 374

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
RVC-CP RD
Sbjct: 254 RVCACPRD 262

>gi|4731632|gb|AA028535.1|AF135121.1 tumor suppressor protein p53 [Homo sapien
Length = 393

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
RVC-CP RD
Sbjct: 273 RVCACPRD 281

>gi|10720195|gb|U09678|p53 BARBU Cellular tumor antigen p53 (Tumor suppressor p
gi|4959050|gb|AA014212.1|AF071570.1 tumor suppressor protein p53 [Barbus barbus]
Length = 369

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
RVC-CP RD
Sbjct: 237 RVCACPRD 245

>gi|223927|ref|U001197A antigen p53, tumor
Length = 390
Score = 25.2 bits (52), Expect = 108

http://www.ncbi.nlm.nih.gov/Blast.cgi

7/10/2003

Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 270 RVCACPGRD 278

>gi|11342599|emb|CAC17147.1| **1** transformation related protein 53 [Mus musculus]
Length = 307

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 270 RVCACPGRD 278

>gi|1885503|ref|NP_571402.1| **1** tumor protein p53; tumor suppressor homolog p53; antigen p53 [Danio rerio]
gi|2829677|sp|P79734|P53_BRARE Cellular tumor antigen p53 (Tumor suppressor p53)
gi|1778019|gb|AA040612.1| **1** tumor suppressor p53 [Danio rerio]
Length = 373

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 241 RVCACPGRD 249

>gi|120720186|sp|O99MB2|P53_PIG Cellular tumor antigen p53 (Tumor suppressor p53)
gi|6185623|gb|AA04620.1|AF096067.1 tumor suppressor p53 (Sus scrofa)
Length = 386

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 266 RVCACPGRD 274

>gi|2829194|gb|AAC26190.1| tumor suppressor ortholog [Xiphophorus maculatus]
Length = 153

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 47 RVCACPGRD 55

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

>gi|4996230|dbj|BA078379.1| p53 [Canis familiaris]
Length = 381

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 261 RVCACPGRD 269

>gi|13591878|ref|NP_112251.1| **1** tumor protein p53; tumor protein p53 (Li-Fraumeni syndrome)
norvegicus
gi|205952|gb|AA01788.1| **1** tumor suppressor
Length = 391

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 271 RVCACPGRD 279

>gi|129374|sp|P07193|P53_XENLA Cellular tumor antigen p53 (Tumor suppressor p53)
gi|83718|dbj|AA29376 Cellular tumor antigen p53 - African clawed frog
gi|64962|emb|CAA28821.1| ORF (AA 1-363) [Xenopus laevis]
gi|214640|gb|AA049923.1| p53 protein homologue; putative
Length = 363

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 248 RVCACPGRD 256

>gi|506453|emb|CAA42635.1| **1** p53 transformation suppressor [Homo sapiens]
Length = 393

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 273 RVCACPGRD 281

>gi|5353744|gb|AA042225.1| p53 protein [Canis familiaris]
Length = 246

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 156 RVCACPKRD 164

[>gi|1389675|gb|AA18936.1|] tumor-suppressor [Equus caballus]
Length = 205

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 149 RVCACPKRD 157

[>gi|2961247|gb|AAC05704.1|] **[4]** tumor suppressor p53 [Mus musculus]
Length = 390

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 270 RVCACPKRD 278

[>gi|15175072|gb|AAK94783.1|] **[4]** transformation related protein 53 [Mus musculus]
Length = 391

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 270 RVCACPKRD 278

[>gi|8698972|gb|AAF78533.1|AF223793.1] tumor suppressor p53 [Oncochrychus mykiss]
[gi|8698974|gb|AAF78534.1|AF223794.1] tumor suppressor p53 [Oncochrychus mykiss]
Length = 146

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 42 RVCACPKRD 50

<http://www.ncbi.nlm.nih.gov/blast/blast.cgi>

7/10/2003

[>gi|2897327|gb|AA060156.1|] **[4]** tumor suppressor p53; p53as [Mus musculus]
Length = 381

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 270 RVCACPKRD 278

[>gi|4959056|gb|AA034215.1|AF071573.1] tumor suppressor protein p53 [Oncochrychus]
Length = 265

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 252 RVCACPKRD 260

[>gi|6841071|gb|AAF28891.1|AF124298.1] p53 protein [Sus scrofa]
Length = 387

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 262 RVCACPKRD 270

[>gi|53571|emb|CAA25323.1|] **[4]** p53 [Mus musculus]
Length = 389

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 269 RVCACPKRD 277

[>gi|18997097|gb|AA183290.1|AF475081.1] p53 [Delphinapterus leucas]
Length = 387

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPKRD 9
RVC+CP RD
Sbjct: 267 RVCACPKRD 275

<http://www.ncbi.nlm.nih.gov/blast/blast.cgi>

7/10/2003

>gi|44039818|gb|AK53397.1|AF367373.1 p53 tumor suppressor [Mus musculus]
 Length = 207

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
 RVC+CP RD
 Sbjct: 148 RVCACPRD 156

>gi|28844929|ref|NF_77626.1| p53 tumor suppressor phosphoprotein (Bos taurus)
 gi|2499426|gb|O29628|p53_BOVIN Cellular tumor antigen p53 (Tumor suppressor p53)
 gi|1083096|ref|S51648 cellular tumor antigen p53 - bovine
 gi|602333|emb|CAA57348.1| p53 [Bos taurus]
 gi|1916676|gb|AA51214.1| 53 kDa phosphoprotein [Bos indicus]
 Length = 386

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
 RVC+CP RD
 Sbjct: 266 RVCACPRD 274

>gi|3024331|gb|P56423|p53_MACFA Cellular tumor antigen p53 (Tumor suppressor p53)
 gi|2689467|gb|AA591535.1| p53 [Macaca fascicularis]
 Length = 393

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
 RVC+CP RD
 Sbjct: 273 RVCACPRD 281

>gi|2781308|pdb|1YCS1A S Chain A, p53-53bp2 Complex
 Length = 199

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
 RVC+CP RD
 Sbjct: 180 RVCACPRD 188

>gi|642241|emb|CA25652.1| p53 [Homo sapiens]
 Length = 293

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

Score = 25.2 bits (52), Expect = 108
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 RVCSCPRD 9
 RVC+CP RD
 Sbjct: 173 RVCACPRD 181

Get selected sequences Select all Deselected all

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF
 Posted date: Jul 10, 2003 1:49 AM
 Number of letters in database: 474,244,320
 Number of sequences in database: 1,477,204

Lambda K H
 0.358 0.293 2.10

Gapped
 Lambda K H
 0.294 0.110 0.610

Matrix: PAM30
 Gap Penalties: Existence: 9, Extension: 1
 Number of Hits to DB: 7,962,851
 Number of Sequences: 1477204
 Number of extensions: 43666
 Number of successful extensions: 1286
 Number of sequences better than 20000.0: 100
 Number of HSP's better than 20000.0 without gapping: 1235
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1286
 length of query: 9
 length of database: 474,244,320
 effective HSP length: 0
 effective length of query: 9
 effective length of database: 474,244,320
 effective search space: 4268198880
 effective search space used: 4268198880
 T: 11
 A: 40
 X1: 14 (7.2 bits)
 X2: 35 (14.8 bits)
 X3: 58 (24.6 bits)
 S1: 35 (19.8 bits)
 S2: 35 (18.0 bits)

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1990),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057861714-02581-23117

Query= SEQID26
(9 letters)

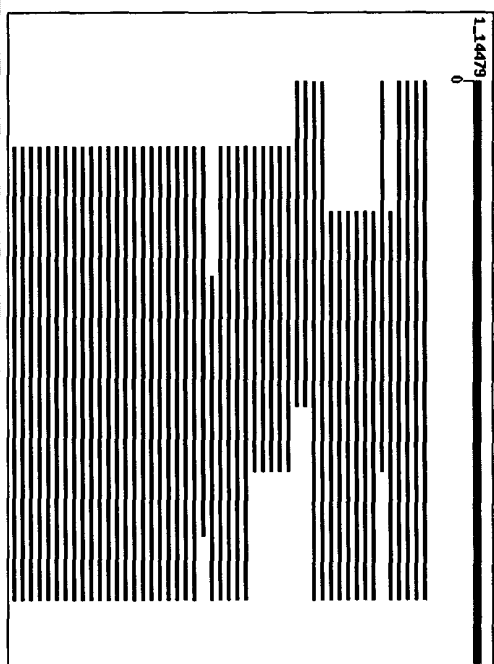
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PIR
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST Page](#)

[Taxonomy reports](#)

Distribution of 111 Blast Hits on the Query Sequence

[Mouse over to show define and scores. Click to show alignments](#)



Related Structures

Sequences producing significant alignments:

	Score	E
	(bits)	Value
gi 31207283 ref XP_312608.1 ENSANGP0000014785 [Anopheles ...	31	1.8
gi 21355617 ref NP_651115.1 CG10873-PA [Drosophila melanog...	29	10
gi 25009887 gb AA071112.1 A28346p [Drosophila melanogaster]	29	10
gi 18150104 dbj BA08367.1 insulin receptor [Paralichthys ...	25	144
gi 23867780 dbj BAC21014.1 claudin4L2 [Xenopus laevis]	25	144
gi 21623719 dbj BAC00941.1 HT-protein [Lycopersicon peruv...	24	260
gi 17227039 gb AA037982.1 A442140.1 scyle-specific self-in...	24	260
gi 21623726 dbj BAC00944.1 HT-A protein [Lycopersicon chmi...	24	260
gi 729929 sp P80424 LDPI_HIRME Leech-derived trypsin inh...	24	260
gi 21623723 dbj BAC00943.1 HT-protein [Lycopersicon parvif...	24	260
gi 21623729 dbj BAC00945.1 HT-A protein [Lycopersicon hirs...	24	260
gi 17227037 gb AA037981.1 A442139.1 scyle-specific self-in...	24	260
gi 8037578 gb AA071401.1 HT-protein [Lycopersicon peruv...	24	260
gi 6957493 gb AA032427.1 A421778.1 tachyzoite serine prote...	24	349
gi 15418693 gb AA091072.1 arrow [Drosophila melanogaster]	24	349
gi 24653390 ref NP_524737.2 arrow CG5912-PA [Drosophila me...	24	349
gi 1673504 emb CAA6181.1 G protein-coupled receptor kinas...	24	349
gi 7513209 pir G02453 NN8-4AG - human (fragment) >gi 12453...	24	349
gi 12621084 ref NP_075217.1 G protein-coupled receptor kin...	24	349
gi 17440180 ref XP_039548.2 similar to NN8-4AG [Homo sapiens]	24	349
gi 6760453 gb AA028358.1 A223365.1 LDL-related protein LRP...	24	349
gi 32451930 gb AA054643.1 unknown (protein for MGC64214) ...	23	468
gi 31205795 ref XP_311845.1 ENSANGP0000018251 [Anopheles ...	23	468

gi 2466447 ref NP_608372.1	CG9572-PA [Drosophila melanoga...	21	468	L
gi 13125045 ref XP_319172.1	ENSANGP0000011831 [Anopheles ...	22	468	
gi 15236812 ref NP_194396.1	expressed protein [Arabidopsis ...	22	468	
gi 2498232 ref Q91713 CHRD_XENLA	Chordin precursor (Organize...	22	843	
gi 129372 ref P10361 P53_RAT	Cellular tumor antigen p53 (tum...	22	1131	L
gi 17259331 dbj BAAB9786.1	p53 [Macaca fasciata]	22	1131	
gi 189479 gb AA59989.1	p53 cellular tumor antigen	22	1131	L
gi 693787 gb AA831269.1	tumor suppressor [Canis familiaris]	22	1131	
gi 8400728 ref NP_000537.2	tumor protein p53 [Homo sapiens...	22	1131	L
gi 4950581 gb AA034216.1 AF071574.1	tumor suppressor protei...	22	1131	
gi 1709531 ref P51664 P53_SHEEP	Cellular tumor antigen p53 (...	22	1131	
gi 129266 ref P04637 P53_HUMAN	Cellular tumor antigen p53 (T...	22	1131	L
gi 183615 gb AA46899.1	sequence-specific transcription f...	22	1131	
gi 11321107 gb AA634052.1	p53 tumor suppressor [Rattus nor...	22	1131	
gi 16266760 dbj BAB69969.1	p53 [Meriones unguiculatus]	22	1131	
gi 12173010 pdb 1GZHC	Chain C, Crystal Structure of the Br...	22	1131	S
gi 6755881 ref NP_035770.1	transformation related protein ...	22	1131	L
gi 200201 gb AA39882.1	p53 [Equus caballus]	22	1131	L
gi 1154648 emb CAA62905.1	p53 [Equus caballus]	22	1131	
gi 3281079 ref NP_012946 P53_PAPPE	Cellular tumor antigen p53 (...	22	1131	
gi 1171969 ref P41685 P53_FETCA	Cellular tumor antigen p53 (...	22	1131	
gi 1000577 gb AA42022.1	p53 [Canis familiaris]	22	1131	
gi 197651 emb CAA62450.1	p53 [Callionymus lyra]	22	1131	
gi 20900490 ref XP_128695.1	similar to transformation rela...	22	1131	L
gi 8698976 gb AA78535.1 AF223795.1	tumor suppressor p53 [On...	22	1131	
gi 1729419 dbj BA08629.1	p53 gene product [Bos primigenius]	22	1131	
gi 4731632 gb AA028535.1 AF135121.1	tumor suppressor protei...	22	1131	L
gi 10720195 ref NP_029678 P53_BARBU	Cellular tumor antigen p53 ...	22	1131	
gi 223827 ref 10011974	antigen p53, tumor	22	1131	
gi 1134259 emb CAC1747.1	transformation related protein ...	22	1131	L
gi 18859503 ref NP_571402.1	tumor protein p53; tumor suppr...	22	1131	L
gi 10720186 ref NP_029678 P53_PIG	Cellular tumor antigen p53 (T...	22	1131	
gi 2829194 gb AA626190.1	tumor suppressor ortholog [Xiphop...	22	1131	
gi 4996220 dbj BA078379.1	p53 [Canis familiaris]	22	1131	
gi 13551878 ref NP_112251.1	tumor protein p53; tumor prote...	22	1131	L
gi 129374 ref P07193 P53_XENLA	Cellular tumor antigen p53 (T...	22	1131	
gi 506453 emb CAA42635.1	p53 transformation suppressor [Ho...	22	1131	L
gi 535744 gb AA042225.1	p53 protein [Canis familiaris]	22	1131	
gi 123491729 dbj BA016799.1	p53 [Homo sapiens]	22	1131	L
gi 1389675 gb AA18936.1	tumor-suppressor [Equus caballus]	22	1131	
gi 2964247 gb AA05704.1	tumor suppressor p53 [Mus musculus]	22	1131	L
gi 15375072 gb AAK94783.1	transformation related protein 5...	22	1131	L
gi 8698972 gb AA78533.1 AF223793.1	tumor suppressor p53 [On...	22	1131	
gi 28975327 gb AA060156.1	tumor suppressor p53; p53as [Mus...	22	1131	L
gi 4935056 gb AA034216.1 AF071573.1	tumor suppressor protei...	22	1131	
gi 6841071 gb AA28897.1 AF124298.1	p53 protein [Sus scrofa]	22	1131	L
gi 153571 emb CAA5233.1	p53 [Mus musculus]	22	1131	
gi 1897097 gb AA183290.1 AF475081.1	p53 [Delphinapterus le...	22	1131	L
gi 14039618 gb AAK5337.1 AF367373.1	p53 tumor suppressor (...	22	1131	L
gi 28849929 ref NP_776626.1	p53 tumor suppressor phosphor...	22	1131	
gi 3024331 ref P54423 P53_MACFA	Cellular tumor antigen p53 (...	22	1131	
gi 2781308 pdb 1VCS A	Chain A, P53-53bp2 Complex	22	1131	S
gi 542241 emb CAA25652.1	p53 [Homo sapiens]	22	1131	L

gi 10720196 ref NP_029678 P53_TERNU	Cellular tumor antigen p53 ...	22	1131	
gi 10720197 ref NP_029678 P53_CAYO	Cellular tumor antigen p53 ...	22	1131	
gi 506444 emb CAA42633.1	p53 transformation suppressor [Ho...	22	1131	L
gi 129366 ref P10360 P53_CHICK	Cellular tumor antigen p53 (T...	22	1131	
gi 1619833 gb AA16961.1	p53 [Canis familiaris]	22	1131	
gi 14719450 pdb 1H08 A	Chain A, Crystal Structure of the Mo...	22	1131	S
gi 506445 emb CAA42633.1	p53 transformation suppressor [Ho...	22	1131	L
gi 5081783 gb AA034216.1 AF151353.1	tumor suppressor p53 [M...	22	1131	L
gi 10720190 ref NP_036006 P53_MARO	Cellular tumor antigen p53 ...	22	1131	
gi 1233855 gb AA92052.1	p53 [Xiphophorus maculatus]	22	1131	
gi 506443 emb CAA42630.1	p53 transformation suppressor [Ho...	22	1131	L
gi 15215061 gb AAH12650.1	Cldn3 protein [Mus musculus]	22	1131	L
gi 12173008 pdb 1GZHA	Chain A, Crystal Structure of the Br...	22	1131	S
gi 339814 gb AA61211.1	p53 antigen	22	1131	L
gi 2842741 ref NP_029533 P53_RABIT	Cellular tumor antigen p53 (...	22	1131	
gi 1733089 gb AA033322.1	cellular phosphoprotein p53	22	1131	
gi 339816 gb AA61212.1	p53 antigen	22	1131	L
gi 10720193 ref NP_029533 P53_XIPWA	Cellular tumor antigen p53 ...	22	1131	L
gi 506444 emb CAA42629.1	p53 transformation suppressor [Ho...	22	1131	L
gi 6031639 ref NP_029537 P53_CAME	Cellular tumor antigen p53 (...	22	1131	
gi 10720192 ref NP_029537 P53_ICPNU	Cellular tumor antigen p53 ...	22	1131	
gi 1463021 gb AA033335.1	p53 [Canis familiaris]	22	1131	
gi 481535 ref NP_029537 P53_ICPNU	Cellular tumor antigen p53, minor sp...	22	1131	L
gi 386994 gb AA033322.1	phosphoprotein p53 [Homo sapiens]	22	1131	L

Alignments

Get selected sequences

Selected all

Deselect all

>gi|121207283|ref|NP_312608.1| ENSANGP0000014785 [Anopheles gambiae str. PEST]
 gi|121295812|gb|AA07957.1| ENSANGP0000014785 [Anopheles gambiae str. PEST]
 Length = 338

Score = 31.2 bits (66), Expect = 1.8
 Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 1 KVCSCPKND 9
 K+CSCKPKND 317

Subject: 309 KVCSCPKND 317

>gi|21355617|ref|NP_651115.1| CG10873-PA [Drosophila melanogaster]
 gi|1721167|gb|AA040427.1|AF224713.1
 gi|1721169|gb|AA040428.1|AF224714.1
 gi|17281624|gb|AA040429.1|AF224715.1
 gi|18272608|gb|AA040430.1|AF224716.1
 gi|18272609|gb|AA040431.1|AF224717.1
 gi|18272610|gb|AA040432.1|AF224718.1
 gi|18272611|gb|AA040433.1|AF224719.1
 gi|18272612|gb|AA040434.1|AF224720.1
 gi|18272613|gb|AA040435.1|AF224721.1
 gi|18272614|gb|AA040436.1|AF224722.1
 gi|18272615|gb|AA040437.1|AF224723.1
 gi|18272616|gb|AA040438.1|AF224724.1
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 gi|18272627|gb|AA040449.1|AF224735.1
 gi|18272628|gb|AA040450.1|AF224736.1
 gi|18272629|gb|AA040451.1|AF224737.1
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 gi|18272633|gb|AA040455.1|AF224741.1
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 gi|18272674|gb|AA040496.1|AF224782.1
 gi|18272675|gb|AA040497.1|AF224783.1
 gi|18272676|gb|AA040498.1|AF224784.1
 gi|18272677|gb|AA040499.1|AF224785.1
 gi|18272678|gb|AA040500.1|AF224786.1
 gi|18272679|gb|AA040501.1|AF224787.1
 gi|18272680|gb|AA040502.1|AF224788.1
 gi|18272681|gb|AA040503.1|AF224789.1
 gi|18272682|gb|AA040504.1|AF224790.1
 gi|18272683|gb|AA040505.1|AF224791.1
 gi|18272684|gb|AA040506.1|AF224792.1
 gi|18272685|gb|AA040507.1|AF224793.1
 gi|18272686|gb|AA040508.1|AF224794.1
 gi|18272687|gb|AA040509.1|AF224795.1
 gi|18272688|gb|AA040510.1|AF224796.1
 gi|18272689|gb|AA040511.1|AF224797.1
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 gi|18272692|gb|AA040514.1|AF224800.1
 gi|18272693|gb|AA040515.1|AF224801.1
 gi|18272694|gb|AA040516.1|AF224802.1
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 gi|18272696|gb|AA040518.1|AF224804.1
 gi|18272697|gb|AA040519.1|AF224805.1
 gi|18272698|gb|AA040520.1|AF224806.1
 gi|18272699|gb|AA040521.1|AF224807.1
 gi|18272700|gb|AA040522.1|AF224808.1
 gi|18272701|gb|AA040523.1|AF224809.1
 gi|18272702|gb|AA040524.1|AF224810.1
 gi|18272703|gb|AA040525.1|AF224811.1
 gi|18272704|gb|AA040526.1|AF224812.1
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 gi|18272708|gb|AA040530.1|AF224816.1
 gi|18272709|gb|AA040531.1|AF224817.1
 gi|18272710|gb|AA040532.1|AF224818.1
 gi|18272711|gb|AA040533.1|AF224819.1
 gi|18272712|gb|AA040534.1|AF224820.1
 gi|18272713|gb|AA040535.1|AF224821.1
 gi|18272714|gb|AA040536.1|AF224822.1
 gi|18272715|gb|AA040537.1|AF224823.1
 gi|18272716|gb|AA040538.1|AF224824.1
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 gi|18272718|gb|AA040540.1|AF224826.1
 gi|18272719|gb|AA040541.1|AF224827.1
 gi|18272720|gb|AA040542.1|AF224828.1
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 gi|18272722|gb|AA040544.1|AF224830.1
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 gi|18272725|gb|AA040547.1|AF224833.1
 gi|18272726|gb|AA040548.1|AF224834.1
 gi|18272727|gb|AA040549.1|AF224835.1
 gi|18272728|gb|AA040550.1|AF224836.1
 gi|18272729|gb|AA040551.1|AF224837.1
 gi|18272730|gb|AA040552.1|AF224838.1
 gi|18272731|gb|AA040553.1|AF224839.1
 gi|18272732|gb|AA040554.1|AF224840.1
 gi|18272733|gb|AA040555.1|AF224841.1
 gi|18272734|gb|AA040556.1|AF224842.1
 gi|18272735|gb|AA040557.1|AF224843.1
 gi|18272736|gb|AA040558.1|AF224844.1
 gi|18272737|gb|AA040559.1|AF224845.1
 gi|18272738|gb|AA040560.1|AF224846.1
 gi|18272739|gb|AA040561.1|AF224847.1
 gi|18272740|gb|AA040562.1|AF224848.1
 gi|18272741|gb|AA040563.1|AF224849.1
 gi|18272742|gb|AA040564.1|AF224850.1
 gi|18272743|gb|AA040565.1|AF224851.1
 gi|18272744|gb|AA040566.1|AF224852.1
 gi|18272745|gb|AA040567.1|AF224853.1
 gi|18272746|gb|AA040568.1|AF224854.1
 gi|18272747|gb|AA040569.1|AF224855.1
 gi|18272748|gb|AA040570.1|AF224856.1
 gi|18272749|gb|AA040571.1|AF224857.1
 gi|18272750|gb|AA040572.1|AF224858.1
 gi|18272751|gb|AA040573.1|AF224859.1
 gi|18272752|gb|AA040574.1|AF224860.1
 gi|18272753|gb|AA040575.1|AF224861.1
 gi|18272754|gb|AA040576.1|AF224862.1
 gi|18272755|gb|AA040577.1|AF224863.1
 gi|18272756|gb|AA040578.1|AF224864.1
 gi|18272757|gb|AA040579.1|AF224865.1
 gi|18272758|gb|AA040580.1|AF224866.1
 gi|18272759|gb|AA040581.1|AF224867.1
 gi|18272760|gb|AA040582.1|AF224868.1
 gi|18272761|gb|AA040583.1|AF224869.1
 gi|18272762|gb|AA040584.1|AF224870.1
 gi|18272763|gb|AA040585.1|AF224871.1
 gi|18272764|gb|AA040586.1|AF224872.1
 gi|18272765|gb|AA040587.1|AF224873.1
 gi|18272766|gb|AA040588.1|AF224874.1
 gi|18272767|gb|AA040589.1|AF224875.1
 gi|18272768|gb|AA040590.1|AF224876.1
 gi|18272769|gb|AA040591.1|AF224877.1
 gi|18272770|gb|AA040592.1|AF224878.1
 gi|18272771|gb|AA040593.1|AF224879.1
 gi|18272772|gb|AA040594.1|AF224880.1
 gi|18272773|gb|AA040595.1|AF224881.1
 gi|18272774|gb|AA040596.1|AF224882.1
 gi|18272775|gb|AA040597.1|AF224883.1
 gi|18272776|gb|AA040598.1|AF224884.1
 gi|18272777|gb|AA040599.1|AF224885.1
 gi|18272778|gb|AA0406

[gi|18032162|gb|AA556639.1|AF192555.1](#) p53-like regulator of apoptosis and cell cyc
melanogaster]
Length = 385

Score = 28.6 bits (60), Expect = 10
Identities = 7/9 (77%), Positives = 9/9 (100%)

Query: 1 KVCSCPKRD 9
K+C+CPKRD
Sbjct: 259 KICCPKRD 267

[gi|25009887|gb|AAW71112.1](#) AT28346p [Drosophila melanogaster]
Length = 519

Score = 28.6 bits (60), Expect = 10
Identities = 7/9 (77%), Positives = 9/9 (100%)

Query: 1 KVCSCPKRD 9
K+C+CPKRD
Sbjct: 393 KICCPKRD 401

[gi|18150104|dbj|BA83667.1](#) insulin receptor [Paralichthys olivaceus]
Length = 1369

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 1 KVCSCPKRD 9
KVC+CPK D
Sbjct: 705 KVCACPKRD 713

[gi|23867780|dbj|BAQ21014.1](#) claudin4L2 [Xenopus laevis]
Length = 213

Score = 24.8 bits (51), Expect = 144
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPCKRD 9
CSCPCKR+
Sbjct: 183 CSCPCKR 189

[gi|21623719|dbj|BAC00941.1](#) HT-protein [Lycopersicon peruvianum]
Length = 96

Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPCKRD 9
CSCPCK+D
Sbjct: 61 CSCPCKD 67

[gi|17227039|gb|AA137982.1|AF442140.1](#) style-specific self-incompatibility putat;
HT-A2 [Solanum chacoense]
Length = 77

Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPCKRD 9
CSCPCK+D
Sbjct: 44 CSCPCKD 50

[gi|21623726|dbj|BAC00944.1](#) HT-A protein [Lycopersicon chmielewskii]
Length = 89

Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPCKRD 9
CSCPCK+D
Sbjct: 55 CSCPCKD 61

[gi|729929|sp|P80424|LDTI_HIRME](#) leech-derived trypsin inhibitor (LDTI)
[gi|7531702|pir|S50015](#) leech-derived trypsin inhibitor - medicinal leech
[gi|3212564|pdb|1LDT|L](#) Chain L, Complex Of leech-Derived Trypsin Inhibitor With
Porcine Trypsin
[gi|3318723|pdb|1AN1|I](#) Chain I, Leech-Derived Trypsin Inhibitor-TRYPSIN COMPLEX
[gi|98917|gb|AA33769.1](#) master cell trypsin inhibitor, LDTI [Hirudo
medicinalis=medical leeches, Peptide, 46 aa]
Length = 46

Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 1 KVCSCPK 7
KVC+CPK
Sbjct: 2 KVCACPK 8

[gi|21623723|dbj|BAC00943.1](#) HT-protein [Lycopersicon parviflorum]
Length = 90

Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 3 CSCPCKRD 9
CSCPCK+D
Sbjct: 55 CSCPCKD 61

[gi|21623729|dbj|BAC00945.1](#) HT-A protein [Lycopersicon hirsutum]

Length = 84

Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)Query: 3 CSCPKD 9
CSCPK+D
Sbjct: 50 CSCPKD 56[>gi|17227037|gb|AAJ37981.1|AF442139.1 style-specific self-incompatibility putat;
HT-A1 (Solanum chacoense)
Length = 99Score = 24.0 bits (49), Expect = 260
Identities = 6/7 (85%), Positives = 7/7 (100%)Query: 3 CSCPKD 9
CSCPK+D
Sbjct: 66 CSCPKD 72[>gi|8037578|gb|AA71401.1| serine proteinase inhibitor (Toxoplasma gondii)
Length = 62Score = 23.5 bits (48), Expect = 349
Identities = 6/6 (100%), Positives = 6/6 (100%)Query: 1 KVCSCP 6
KVCSCP
Sbjct: 21 KVCSCP 26[>gi|6957493|gb|AA732427.1|AF121778.1 tachyzoite serine proteinase inhibitor [To;
Length = 294Score = 23.5 bits (48), Expect = 349
Identities = 6/6 (100%), Positives = 6/6 (100%)Query: 1 KVCSCP 6
KVCSCP
Sbjct: 28 KVCSCP 33[>gi|15418693|gb|AA791072.1| arrow [Drosophila melanogaster]
Length = 1678Score = 23.5 bits (48), Expect = 349
Identities = 6/6 (100%), Positives = 6/6 (100%)Query: 2 VCSCPK 7
VCSCPK
Sbjct: 1297 VCSCPK 1302<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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[>gi|24653390|ref|NP_524737.2| arrow CG5912-PA [Drosophila melanogaster]
gi|21627234|gb|AA758373.2| CG5912-PA [Drosophila melanogaster]
Length = 1678Score = 23.5 bits (48), Expect = 349
Identities = 6/6 (100%), Positives = 6/6 (100%)Query: 2 VCSCPK 7
VCSCPK
Sbjct: 1297 VCSCPK 1302[>gi|1673504|emb|CA66181.1| G protein-coupled receptor kinase GRK4B [Rattus nu;
Length = 544Score = 23.5 bits (48), Expect = 349
Identities = 7/12 (58%), Positives = 9/12 (75%), Gaps = 3/12 (25%)Query: 1 KVCSC---PKRD 9
K+CSC PKR+
Sbjct: 508 KICSCILRPKN 519[>gi|7513209|pir|G02453 NN8-4AG - human (fragment)
gi|1245372|gb|AA838131.1| NN8-4AG
Length = 412Score = 23.5 bits (48), Expect = 349
Identities = 6/6 (100%), Positives = 6/6 (100%)Query: 2 VCSCPK 7
VCSCPK
Sbjct: 369 VCSCPK 374[>gi|12621084|ref|NP_075217.1| G protein-coupled receptor kinase 2, groucho ge;
norvegicus)
gi|1673503|emb|CA66180.1| G protein-coupled receptor kinase GRK4A [Rattus norv;
Length = 575Score = 23.5 bits (48), Expect = 349
Identities = 7/12 (58%), Positives = 9/12 (75%), Gaps = 3/12 (25%)Query: 1 KVCSC---PKRD 9
K+CSC PKR+
Sbjct: 539 KICSCILRPKN 550[>gi|17440180|ref|XP_039548.2| similar to NN8-4AG [Homo sapiens]
Length = 418

Score = 23.5 bits (48), Expect = 349

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCSCP 7

Sbjct: 375 VCSCP 380

>gi|6760453|gb|AA28358.1|AF223365.1 LDU-related protein LRP6 [Drosophila mel;]
Length = 1678

Score = 23.5 bits (48), Expect = 349
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCSCP 7

Sbjct: 1297 VCSCP 1302

>gi|32451930|gb|AAH54643.1 Unknown (protein for WGC:64214) [Danio rerio]
Length = 579

Score = 23.1 bits (47), Expect = 468
Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 2/10 (20%)

Query: 2 VCSCP-KRD 9

Sbjct: 46 VCSCP KR+ 55

>gi|31205795|ref|XP_311849.1 ENSANGP0000018251 [Anopheles gambiae]
gi|30177281|gb|AA07856.2 ENSANGP0000018251 [Anopheles gambiae str. PEST]
Length = 465

Score = 23.1 bits (47), Expect = 468
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 1/8 (12%)

Query: 2 VCSCP-KRD 9

Sbjct: 324 VCSCP-RD 330

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

Sbjct: 164 VCSCP 168

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

VCSCP

Sbjct: 105 VCSCP 109

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 2 VCSCP 7

Sbjct: 265 VCSCP 270

Score = 18.0 bits (35), Expect = 15950
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

Sbjct: 431 VCSCP 435

Score = 18.0 bits (35), Expect = 15950
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

Sbjct: 372 VCSCP 376

>gi|24643447|ref|NP_608372.1 CG9572-PA [Drosophila melanogaster]
gi|7289281|gb|AA45359.1 CG9572-PA [Drosophila melanogaster]
Length = 441

Score = 23.1 bits (47), Expect = 468
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 1/8 (12%)

Query: 2 VCSCP-KRD 9

Sbjct: 307 VCSCP-RD 313

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

Sbjct: 146 VCSCP 150

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

Sbjct: 87 VCSCP 91

Score = 19.3 bits (38), Expect = 6602
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 2 VCSCP 7

Sbjct: 248 VCCECP 253

[>gi|31235045|ref|XP_319172.1| ENSANGP0000011831 [Anopheles gambiae]
gi|21301731|gb|EAA13876.1| ENSANGP0000011831 [Anopheles gambiae str. FESST]
Length = 2212

Score = 23.1 bits (47), Expect = 468
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 1/8 (12%)

Query: 2 VCSCPRD 9

Sbjct: 100 VCSCP RD 106

Score = 21.0 bits (42), Expect = 2037
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCSCPR 8

Sbjct: 188 VCSCPAR 194

Score = 18.5 bits (36), Expect = 11887
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

Sbjct: 514 ICSCP 518

Score = 18.0 bits (35), Expect = 15950
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 VCSCP 6

Sbjct: 903 VCNCP 907

[>gi|15236812|ref|NP_194396.1| expressed protein [Arabidopsis thaliana]
gi|7487040|pir|T08932.1| hypothetical protein T15M24.110 - Arabidopsis thaliana
gi|4398504|emb|CAB3862.1| putative protein [Arabidopsis thaliana]
gi|7269518|emb|CAI79521.1| putative protein [Arabidopsis thaliana]
Length = 806

Score = 23.1 bits (47), Expect = 468

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 4 SCPRD 9

Sbjct: 184 SCPRD 189

[>gi|2498235|sp|Q91713|CHRD_XENLA Chordin precursor [Organizer-specific secreted
gi|1072455|pir|A55195 chordin precursor - African clawed frog
gi|603945|gb|AAC42222.1| chordin
Length = 941

Score = 22.3 bits (45), Expect = 843
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCSCPR 8

Sbjct: 716 VCSCQR 722

[>gi|129372|sp|P10361|P53_RAT Cellular tumor antigen p53 (tumor suppressor p53)
gi|92070|pir|S02192 cellular tumor antigen p53 - rat
gi|56829|emb|CAA31457.1| nuclear protein p53 (AA 1 - 391) [Rattus norvegicus]
Length = 391

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9

Sbjct: 272 VCACPRD 279

[>gi|1259331|db|BA92786.1| P53 [Macaca fuscata]
Length = 181

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9

Sbjct: 149 VCACPRD 156

[>gi|189479|gb|AA59989.1| P53 cellular tumor antigen
Length = 393

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9

Sbjct: 274 VCACPRD 281

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

>gi|693287|gb|AA81269.1| tumour suppressor (Canis familiaris)

Length = 32

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9

VC+CP RD
Sbjct: 5 VCACPRD 12

>gi|8400738|ref|NP_000537.2| tumor protein p53 (Homo sapiens)

gi|625300|pir|IDNHU53 cellular tumor antigen p53 [validated] - human

gi|35214|emb|CAA8095.1| protein p53 (Homo sapiens)

gi|506437|emb|CAA2627.1| p53 transformation suppressor (Homo sapiens)

gi|3041867|gb|AAC12971.1| p53 (Homo sapiens)

gi|473147|gb|AAD8628.1|AF136771.1 tumor suppressor protein p53 (Homo sapiens)

gi|11066970|gb|AA626785.1|AF307851.1 p53 protein (Homo sapiens)

Length = 393

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9

VC+CP RD
Sbjct: 274 VCACPRD 281

>gi|4959058|gb|AAD34216.1|AF071574.1 tumour suppressor protein p53 (Oncomorphus)

Length = 265

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9

VC+CP RD
Sbjct: 253 VCACPRD 260

>gi|1709531|sp|P51664|P53_SHEEP Cellular tumor antigen p53 (Tumor suppressor p53)

Length = 382

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9

VC+CP RD
Sbjct: 263 VCACPRD 270

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

>gi|129369|sp|P04637|P53_HUMAN Cellular tumor antigen p53 (Tumor suppressor p53) (Antigen NY-CO-13)

gi|35210|emb|CAA26306.1| p53 tumor antigen (aa 1-7) (Homo sapiens)

gi|189476|gb|AA59988.1| phosphoprotein p53

gi|7595312|gb|AA64408.1|AF192534.1 tumor suppressor protein p53 [Expression vect

Length = 393

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9

VC+CP RD
Sbjct: 274 VCACPRD 281

>gi|1836145|gb|AA64689.1| sequence-specific transcription factor [Equidae]

Length = 263

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9

VC+CP RD
Sbjct: 225 VCACPRD 232

>gi|11321107|gb|AA634052.1| p53 tumor suppressor (Rattus norvegicus)

Length = 53

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9

VC+CP RD
Sbjct: 13 VCACPRD 20

>gi|1626760|dbj|BA69969.1| p53 [Meriones unguiculatus]

Length = 390

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9

VC+CP RD
Sbjct: 272 VCACPRD 279

>gi|21730310|pdb|1GZM|C Chain C, Crystal Structure of The Bcr1 Domains Of Hum

To The P53 Tumor Suppressor

Length = 198

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 180 VCACPRD 187

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 271 VCACPRD 278

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 271 VCACPRD 278

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 271 VCACPRD 278

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 141 VCACPRD 148

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 249 VCACPRD 256

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi

7/10/2003

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 267 VCACPRD 274

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 267 VCACPRD 274

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 238 VCACPRD 245

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 238 VCACPRD 245

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 38 VCACPRD 45

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 38 VCACPRD 45

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 115 VCACPRD 122

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 115 VCACPRD 122

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)
Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 115 VCACPRD 122

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi

7/10/2003

g1|8698994|gb|AA78544.1|AF223804.1 tumor suppressor p53 [oncorhynchus tshawytscha
g2|8698996|gb|AA78545.1|AF223805.1 tumor suppressor p53 [oncorhynchus tshawytscha
g3|8698998|gb|AA78546.1|AF223806.1 tumor suppressor p53 [oncorhynchus tshawytscha
g4|8699000|gb|AA78547.1|AF223807.1 tumor suppressor p53 [oncorhynchus tshawytscha
g5|8699002|gb|AA78548.1|AF223808.1 tumor suppressor p53 [oncorhynchus tshawytscha
g6|8699004|gb|AA78549.1|AF223809.1 tumor suppressor p53 [oncorhynchus tshawytscha
g7|8699006|gb|AA78550.1|AF223810.1 tumor suppressor p53 [oncorhynchus tshawytscha
g8|8699008|gb|AA78551.1|AF223811.1 tumor suppressor p53 [oncorhynchus tshawytscha
g9|8699010|gb|AA78552.1|AF223812.1 tumor suppressor p53 [oncorhynchus tshawytscha
g10|8699012|gb|AA78553.1|AF223813.1 tumor suppressor p53 [oncorhynchus tshawytscha
g11|8699014|gb|AA78554.1|AF223814.1 tumor suppressor p53 [oncorhynchus tshawytscha
g12|8699016|gb|AA78555.1|AF223815.1 tumor suppressor p53 [oncorhynchus tshawytscha
g13|8699018|gb|AA78556.1|AF223816.1 tumor suppressor p53 [oncorhynchus tshawytscha
g14|8699020|gb|AA78557.1|AF223817.1 tumor suppressor p53 [oncorhynchus tshawytscha
g15|8699022|gb|AA78558.1|AF223818.1 tumor suppressor p53 [oncorhynchus tshawytscha
Length = 146

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 43 VCACPRD 50

>g1|1729419|dbj|BAA08629.1 p53 gene product [Bos primigenius]
Length = 374

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 255 VCACPRD 262

>g1|4731632|gb|AA028535.1|AF35121.1 tumor suppressor protein p53 [Homo sapiens]
Length = 393

Score = 21.8 bits (44), Expect = 1131
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 2 VCSCPRD 9
VC+CP RD
Sbjct: 274 VCACPRD 281

Get selected sequences Select all Deselect all

Database: All non-redundant Genbank CDS
translations+PDB+SwissProt+PIR+PFR
Posted date: Jul 10, 2003 1:49 AM
Number of letters in database: 474,244,320

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi

7/10/2003

Number of sequences in database: 1,477,204
Lambda K H
0.361 0.293 2.09
Gapped
Lambda K H
0.294 0.110 0.610
Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of Hits to DB: 7,988,641
Number of Sequences: 1477204
Number of extensions: 38359
Number of successful extensions: 1191
Number of sequences better than 20000.0: 100
Number of HSP's better than 20000.0 without gapping: 1132
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1191
Length of query: 9
Length of database: 474,244,320
effective HSP length: 0
effective length of query: 9
effective length of database: 474,244,320
effective search space: 4268198880
effective search space used: 4268198880
t: 11
A: 40
X1: 14 (7.3 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 35 (20.0 bits)
S2: 35 (18.0 bits)

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi

7/10/2003



results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

RID: 1057869455-01002-4505

Query: SEQID27
(9 letters)

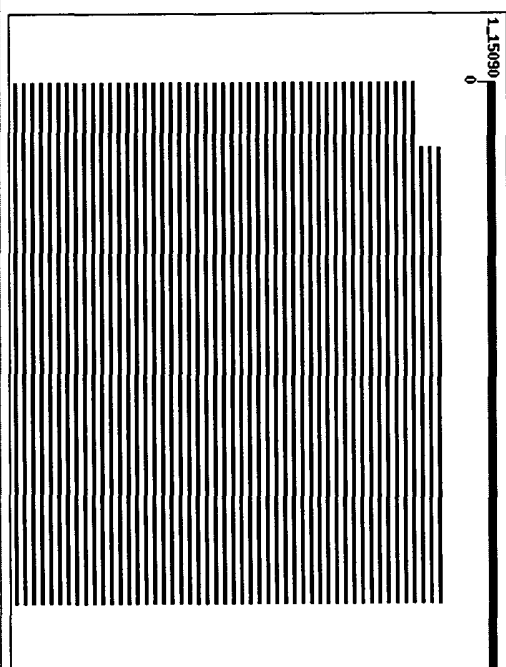
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQ](#)

[Taxonomy reports](#)

Distribution of 112 Blast Hits on the Query Sequence

[Mouse-over to show details and scores. Click to show alignments](#)



Sequences producing significant alignments:

	Score	E
	(bits)	Value
g1 21355617 ref NP_651115.1 CG10873-PA [Drosophila melanogaster]...	31	1.8
g1 25009887 gb AAAT71112.1 AT28146p [Drosophila melanogaster]...	31	1.8
g1 31207283 ref XP_312608.1 ENSANGP00000014785 [Anopheles ...]	28	14
g1 3695096 gb AAC62642.1 DN p63 gamma [Mus musculus]	25	108
g1 13751181 emb CAC37102.1 DN KET gamma protein [Rattus no...	25	108
g1 13751173 emb CAC37098.1 TAI KET alpha protein [Rattus n...	25	108
g1 20428532 gb AAK81886.1 DN p73 gamma [Homo sapiens]	25	108
g1 1813451 gb AA841833.1 p53	25	108
g1 19909983 db BAB87245.1 deltan p73 beta [Homo sapiens] ...	25	108
g1 7248451 gb AA843492.1 p51 isoform delbeta [Homo sapiens]	25	108
g1 20892181 ref XP_147232.1 transformation related protein...	25	108
g1 3695094 gb AAC62641.1 TA*P63 alpha [Mus musculus]	25	108
g1 12060406 db BAB20591.1 delta N p73l [Homo sapiens]	25	108
g1 4803651 emb CAA72225.1 p73 splice variant [Cercopithecu...	25	108
g1 13751179 emb CAC37101.1 TA2 KET gamma protein [Rattus n...	25	108
g1 15072750 emb CAC48053.1 p63 delta [Homo sapiens]	25	108
g1 29470179 gb AA074632.1 p73 (Danio rerio)	25	108
g1 2581764 gb AA882420.1 p53 (Cricetulus griseus)	25	108
g1 8217484 emb CAB97242.1 dJ1092A11.2 (tumor protein p73) ...	25	108
g1 2370178 emb CAA72221.1 second splice variant [Homo sapi...	25	108
g1 21264484 sp P79820 P53 ORYDA Cellular tumor antigen p53 ...	25	108
g1 1184759 gb AA87577.1 p53 tumor suppressor homolog	25	108
g1 1184757 gb AA87576.1 p53 tumor suppressor homolog	25	108
g1 7248450 gb AA843491.1 p51 isoform delalpha [Homo sapiens]	25	108

gi 1728447 gb AA64488.1	p51 isoform 7A63beta [Homo sapiens]	25	108	
gi 3237375 gb AAC24830.1	p53 homolog [Homo sapiens]	25	108	
gi 475579 gb AA641344.1	tumor suppressor p53 [Mesocricetus ...]	25	108	
gi 27527172 emb CA010682.1	p53 protein [Monodelphis domestica ...]	25	108	
gi 12024746 gb AA645609.1	TA p63 gamma [Homo sapiens]	25	108	
gi 3695086 gb AAC62637.1	TA p63 beta [Homo sapiens]	25	108	
gi 4669098 gb AA027752.1	DN p63 beta [Mus musculus]	25	108	
gi 675883 ref NP_035771.1	transformation related protein ...	25	108	
gi 1244762 gb AA958563.1	p53 tumor suppressor homolog	25	108	
gi 13751187 emb CAC37105.1	DN KET beta protein [Rattus nor...	25	108	
gi 13751175 emb CAC3709.1	DN KET alpha protein [Rattus no...	25	108	
gi 23308709 ref NP_694518.1	deltaNp63 isoform alpha 1, tum...	25	108	
gi 26339452 gb BAC33397.1	unamed protein product [Mus mu...	25	108	
gi 12330871 ref NP_694519.1	deltaNp63 isoform gamma; tumor...	25	108	
gi 3695082 gb AAC62635.1	TA p63 alpha [Homo sapiens]	25	108	
gi 1688502 gb AAC60146.1	p53 [Oryzias latipes] >gi 1208249...	25	108	
gi 20850793 ref XP_131858.1	transformation related protein...	25	108	
gi 13195250 gb AAK15622.1	p63 DNA binding protei...	25	108	
gi 3510328 gb BAA32592.1	p51A [Homo sapiens] >gi 1695078 ...	25	108	
gi 13751185 emb CAC37104.1	TA1 KET beta protein [Rattus no...	25	108	
gi 451931 gb AAA7086.1	tumor suppressor protein [Mesocric...	25	108	
gi 1813453 gb BAA41832.1	p53	25	108	
gi 3695080 gb AAC62634.1	DN p63 gamma [Homo sapiens] >gi 7...	25	108	
gi 1813451 gb BAA41831.1	p53	25	108	
gi 397071 emb CAA76562.1	KET protein [Homo sapiens]	25	108	
gi 23308685 ref NP_689454.1	deltaNp63 isoform alpha 2, tum...	25	108	
gi 3445484 gb BAA32433.1	p73H [Homo sapiens]	25	108	
gi 17689271 gb AA67733.1	p53 tumor suppressor-1i...	25	108	
gi 17983567 gb AA650211.1	tumor protein [Canis familiaris]	25	108	
gi 31543181 ref NP_003713.3	tumor protein p73-like; tumor ...	25	108	
gi 19909891 gb BAA87244.1	deltaN p73 alpha [Homo sapiens] ...	25	108	
gi 4101545 gb AAC01196.1	tumor suppressor protein p53 [Ory...	25	108	
gi 1813457 gb BAA41834.1	p53	25	108	
gi 1244764 gb AA698564.1	p53 tumor suppressor homolog	25	108	
gi 17440008 gb J06176	tumor suppressor protein p53 - Chine...	25	108	
gi 12856636 gb BAA30732.1	unamed protein product [Mus mu...	25	108	
gi 19850152 gb AA129584.1	p53-like transcription...	25	108	
gi 17320915 emb CA881954.1	p73 delta-N protein [Mus musculus]	25	108	
gi 1293707 gb J000366 P53_MESAV	Cellular tumor antigen p53 (T...	25	108	
gi 17689273 gb AA67734.1	p73-like protein [Mya a...	25	108	
gi 3695088 gb AAC62638.1	DN p63 beta [Homo sapiens] >gi 12...	25	108	
gi 12301017 emb CAA72219.1	first splice variant [Homo sapiens]	25	108	
gi 35303301 gb BAA32593.1	p51B [Homo sapiens] >gi 17248446 ...	25	108	
gi 1890357 emb CAA70109.1	p53 tumour suppressor [Cricetulu...	25	108	
gi 17284452 gb AA643489.1	p51 isoform deltaNdelta [Homo sapiens]	25	108	
gi 12060487 gb BAA20631.1	DN p63 alpha [Gallus gallus]	25	108	
gi 3695092 gb AAC62640.1	TA*p63 beta [Mus musculus]	25	108	
gi 10720194 gb J097FAL P51_TUPED	Cellular tumor antigen p53 ...	25	108	
gi 17284488 gb AA643489.1	p51 isoform 7A63delta [Homo sapi...	25	108	
gi 3695090 gb AAC62639.1	TA*p63 gamma [Mus musculus]	25	108	
gi 12494281 gb J09185 P53_CRICK	Cellular tumor antigen p53 (...)	25	108	
gi 12643523 gb J093SK8 P73_CERAE	tumor protein p73 [p53-like...	25	108	

gi 4885645 ref NP_005418.1	tumor protein p73; p53-related ...	25	108	
gi 12024745 gb AA645608.1	TA p63 beta [Homo sapiens]	25	108	
gi 9507209 ref NP_062094.1	transformation related protein ...	25	108	
gi 3695086 gb AAC62637.1	TA p63 beta [Homo sapiens]	25	108	
gi 4887145 gb AAC32213.1	p73 [Mus musculus]	25	108	
gi 13751183 emb CAC37103.1	TA2 KET beta protein [Rattus no...	25	108	
gi 3644040 gb AAC43038.1	CUSP [Homo sapiens] >gi 3695084 g...	25	108	
gi 13751177 emb CAC37100.1	TA1 KET gamma protein [Rattus n...	25	108	
gi 22933563 ref NP_00038140.1	hypothetical protein [Xylo...	25	144	
gi 1582472 gb AA109310.1	death receptor 6 [Salv...	25	144	
gi 1352528 gb J01705 WTC1_MOUSE	Neurogenic locus notch homo...	25	144	
gi 17093351 gb F21783 NOTCH_XENLA	Neurogenic locus notch prot...	24	194	
gi 18859115 ref NP_571516.1	notch homolog 1a; neurogenic 1...	24	194	
gi 2765874 ref XP_228135.1	similar to 40kDa ribosomal pro...	24	194	
gi 104252 gb AA5844	Xotch protein - African clawed frog	24	194	
gi 22966887 ref NP_00014482.1	hypothetical protein [Rhodos...	23	468	
gi 8928081 gb J092A11 BHL_RHORU	Aldehyde dehydrogenase >gi ...	23	468	
gi 21238945 gb BAA96577.1	aldehyde dehydrogenase [Cytopha...	23	468	
gi 23113187 ref NP_00098587.1	hypothetical protein [Desul...	23	468	
gi 129337 gb P10361 P53_RAT	Cellular tumor antigen p53 (Tum...	23	628	
gi 7259311 gb BAA92786.1	p53 [Macaca fuscata]	23	628	
gi 692787 gb BAA31269.1	tumor suppressor [Canis familiaris]	23	628	
gi 8400738 ref NP_000537.2	tumor protein p53 [Homo sapiens...	23	628	
gi 4959058 gb AAC34216.1	tumor suppressor protei...	23	628	

Alignments

Get selected sequences Selected all Deselect all

>gi 21355617 ref NP_651115.1	CG10873-PA [Drosophila melanogaster]
gi 1721167 gb AA67427.1	transcription factor p53 [Drosophila melano]
gi 1721169 gb AA67428.1	transcription factor p53 [Drosophila melano]
gi 1781624 gb AA675172.1	p53 tumor suppressor-like protein [Drosophi...
gi 18272608 gb AA674277.1	transcription factor [Drosophila melanogast...
gi 18453176 gb AA675270.1	transcription factor p53 [Drosophila melano]
gi 10726710 gb AA6756087.2	CG10873-PA [Drosophila melanogaster]
gi 17861528 gb AA6739241.1	GHI1591p [Drosophila melanogaster]
gi 18033162 gb AA675639.1	p53-like regulator of apoptosis and cell cyc

Length = 385

Score = 31.2 bits (66), Expect = 1.8
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 ICNCPKD 9
ICNCPKD 9
Sbjct: 260 ICNCPKD 267

[\[>gi|25009887|gb|AAW7112.1\]](#) [AT28346p](#) [*Drosophila melanogaster*]
Length = 519

Score = 31.2 bits (66), Expect = 1.8
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query: 2 ICPCPRD 9
ICPCPRD
Sbjct: 394 ICPCPRD 401

[\[>gi|31207283|ref|XP_312608.1\]](#) [ENSANGP00000014785](#) [*Anopheles gambiae*]
[gi|21295812|gb|EAA07957.1\]](#) [ENSANGP00000014785](#) [*Anopheles gambiae* str. PESTN]
Length = 338

Score = 28.2 bits (59), Expect = 14
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 2 ICPCPRD 9
IC-CPRD
Sbjct: 310 ICSCPRD 317

[\[>gi|3695096|gb|AAC62642.1\]](#) [\[DN p63 gamma](#) [*Mus musculus*]
Length = 389

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 249 RICACPRD 257

[\[>gi|13751181|emb|CAC37102.1\]](#) [\[DN KET gamma protein](#) [*Rattus norvegicus*]
Length = 393

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 249 RICACPRD 257

[\[>gi|13751173|emb|CAC37098.1\]](#) [\[TAI KET alpha protein](#) [*Rattus norvegicus*]
Length = 663

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 326 RICACPRD 334

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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[\[>gi|20428532|gb|AAK81886.1\]](#) [\[DN p73 gamma](#) [*Homo sapiens*]
Length = 426

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 244 RICACPRD 252

[\[>gi|1813455|gb|AA841833.1\]](#) [p53](#)
Length = 238

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 166 RICACPRD 174

[\[>gi|1990983|dbj|BA87245.1\]](#) [\[DN p73 beta](#) [*Homo sapiens*]
[gi|20428530|gb|AAK1885.1\]](#) [\[DN p73 beta](#) [*Homo sapiens*]
Length = 450

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 244 RICACPRD 252

[\[>gi|7248451|gb|AA43492.1\]](#) [p51 isoform delnbeta](#) [*Homo sapiens*]
Length = 461

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 249 RICACPRD 257

[\[>gi|20892181|ref|XP_147232.1\]](#) [\[transformation related protein 63](#) [*Mus musculus*]
Length = 465

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 128 RICACPRGD 136

gi|3695094|gb|AAC62641.1 TA* ρ 63 alpha [Mus musculus]
Length = 680

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 343 RICACPRGD 351

gi|12060406|dbj|BAB20591.1 delta N p73L [Homo sapiens]
Length = 501

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 164 RICACPRGD 172

gi|4803651|emb|CAA72225.1 p73 splice variant [Cercopithecus aethiops]
Length = 499

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 293 RICACPRGD 301

gi|13751179|emb|CAC37101.1 TA2 KET gamma protein [Rattus norvegicus]
Length = 487

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 343 RICACPRGD 351

gi|15072750|emb|CAC48053.1 p63 delta [Homo sapiens]
Length = 232

Score = 25.2 bits (52), Expect = 108

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 191 RICACPRGD 199

gi|29470179|gb|AA074632.1 p73 [Danio rerio]
Length = 640

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 300 RICACPRGD 308

gi|2581764|gb|BAB2420.1 p53 [Cricketulus griseus]
Length = 205

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 148 RICACPRGD 156

gi|8217484|emb|CAB92742.1 DJ1092A11.2 (tumor protein p73) [Homo sapiens]
Length = 661

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 318 RICACPRGD 326

gi|2370178|emb|CAA72221.1 second splice variant [Homo sapiens]
Length = 588

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 245 RICACPRGD 253

gi|21264484|sp|P79820|P53_ORYLA Cellular tumor antigen p53 (Tumor suppressor p53; gi|4101544|gb|ABD01195.1) tumor suppressor protein p53 [Oryzias latipes]

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Length = 352

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 254 RICACPRD 262[>gi|1184759|gb|AA87577.1| p53 tumor suppressor homolog
Length = 189Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 89 RICACPRD 97[>gi|1184757|gb|AA87576.1| p53 tumor suppressor homolog
Length = 228Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 97 RICACPRD 105[>gi|7248450|gb|AA87449.1| p51 isoform delAlpha [Homo sapiens]
Length = 586Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 RICACPRD 257[>gi|7248447|gb|AA87448.1| p51 isoform TAp63beta [Homo sapiens]
Length = 516Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 304 RICACPRD 312<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

[>gi|3273745|gb|AC24830.1| p53 homolog [Homo sapiens]
Length = 356Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 RICACPRD 257[>gi|473579|gb|AA84344.1| tumor suppressor p53 [Mesocricetus auratus]
Length = 396Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 276 RICACPRD 284[>gi|27527128|emb|CD10682.1| p53 protein [Monodelphis domestica]
Length = 238Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 145 RICACPRD 153[>gi|12024746|gb|AA845609.1| pA p63 gamma [Homo sapiens]
Length = 487Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 343 RICACPRD 351[>gi|3695098|gb|AC62643.1| DN p63 beta [Mus musculus]
Length = 461Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 RICACPRD 257<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 301 R1CACPRGD 309

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 301 R1CACPRGD 309

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 R1CACPRGD 257

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 R1CACPRGD 257

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 298 R1CACPRGD 306

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 298 R1CACPRGD 306

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 R1CACPRGD 257

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 R1CACPRGD 257

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 R1CACPRGD 257

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 R1CACPRGD 257

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 R1CACPRGD 257

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 R1CACPRGD 257

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 247 R1CACPRGD 255

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 R1CACPRGD 257

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 249 R1CACPRGD 257

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 247 R1CACPRGD 255

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 247 R1CACPRGD 255

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 304 R1CACPRGD 312

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 304 R1CACPRGD 312

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 304 R1CACPRGD 312

Query: 1 RICTCPKRD 9
RIC CP RD
Sbjct: 304 R1CACPRGD 312

7/10/2003

gi|12082495|gb|AA648557.1|AF212997.1 p53 tumor suppressor (Oryzias latipes)
Length = 351

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 253 RICACPRGD 261

>gi|20850793|ref|XP_131858.1| transformation related protein 73 [Mus musculus]
gi|30794514|ref|NP_035772.1| P73 transformation related protein 73 [Mus musculus]
gi|15209244|emb|CA81953.1| P73 alpha protein [Mus musculus]
Length = 631

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 285 RICACPRGD 293

>gi|13195250|gb|AAK15622.1|AF314148.1 p63 DNA binding protein [Xenopus laevis]
Length = 365

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 249 RICACPRGD 257

>gi|3510328|dbj|BA32592.1| p51A [Homo sapiens]
gi|3695078|gb|AAC62633.1| TA p63 gamma [Homo sapiens]
gi|7248445|gb|AAFA3486.1| p51 isoform TAp63gamma [Homo sapiens]
Length = 448

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 304 RICACPRGD 312

>gi|13751185|emb|CAC37104.1| TAI KET beta protein [Rattus norvegicus]
Length = 538

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

<http://www.ncbi.nlm.nih.gov/blast/blast.cgi>

7/10/2003

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 326 RICACPRGD 334

>gi|451931|gb|AA37086.1| tumor suppressor protein [Mesocricetus auratus]
Length = 206

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 148 RICACPRGD 156

>gi|1813453|gb|AA841832.1| p53
Length = 286

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 166 RICACPRGD 174

>gi|3695080|gb|AAC62634.1| DN p63 gamma [Homo sapiens]
gi|7248449|gb|AAFA3490.1| p51 isoform delngamma [Homo sapiens]
gi|12024749|gb|AA645612.1| DN p63 gamma [Homo sapiens]
Length = 393

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 249 RICACPRGD 257

>gi|1813451|gb|AA841831.1| p53
Length = 378

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 258 RICACPRGD 266

>gi|3970717|emb|CA376562.1| KET protein [Homo sapiens]
Length = 680

<http://www.ncbi.nlm.nih.gov/blast/blast.cgi>

7/10/2003

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 343 RICACPRKD 351

[>gi|23308695|ref|NP_689454.1|] deltanp63 isoform alpha 2; tumor protein p63 [D:
gi|21326973|gb|AA048108.1|AF487944.1] deltan p63 alpha [Danio rerio]
gi|22652333|gb|AA03691.1|AF412284.1] DN p63 alpha 2 [Danio rerio]
Length = 576

Score = 25.2 bits (52), Expect = 108
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RICCPKRD 9
RIC CP RD
Sbjct: 247 RICACPRKD 255

Get selected sequences Select all Deselect all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PPF
Posted date: Jul 10, 2003 1:49 AM
Number of letters in database: 474,244,320
Number of sequences in database: 1,477,204

Lambda K H
0.354 0.293 2.12

Gapped K H
Lambda K H
0.294 0.110 0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of Hits to DB: 7,525,701
Number of Sequences: 1477204
Number of extensions: 33882
Number of successful extensions: 2403
Number of sequences better than 20000.0: 100
Number of HSP's better than 20000.0 without gapping: 2193
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2403
length of query: 9
length of database: 474,244,320
effective HSP length: 0
effective length of query: 9
effective length of database: 474,244,320

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

effective search space: 4268198880
effective search space used: 4268198880
T: 11

A: 40
X1: 14 (7.2 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 35 (19.6 bits)
S2: 35 (18.0 bits)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003



RESULTS of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057869726-06677-18835

Query= SEQID29

(9 letters)

Database: All non-redundant Genbank CDS
Translations+PDB+SwissProt+PIR+PRF
1,477,204 sequences; 474,244,320 total letters

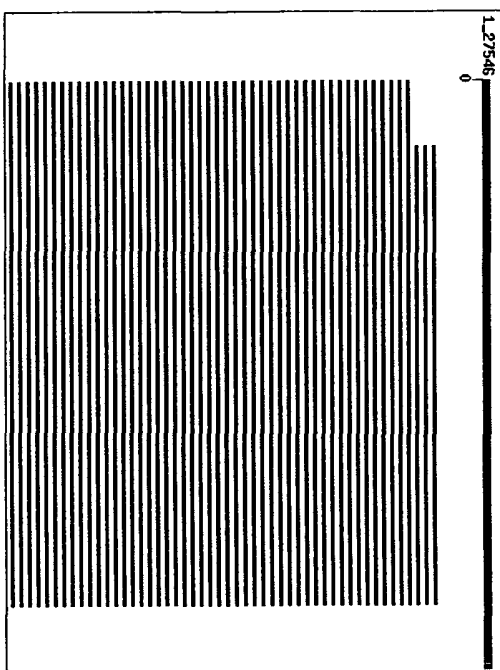
If you have any problems or questions with the results of this search
please refer to the [BLAST FAQ](#)

[Taxonomy reports](#)

Distribution of 101 Blast Hits on the Query Sequence

[Mouse-over to show define and scores. Click to show alignments](#)<http://www.ncbi.nlm.nih.gov/Blast/Blast.cgi>

7/10/2003



Related Structures

Sequences producing significant alignments:

	Score	E
	(bits)	Value
g1 21355617 ref NP_651115.1 CG10873-PA (Drosophila melanogaster)...	29	10
g1 25009887 gb AA71112.1 AT28346p (Drosophila melanogaster)	29	10
g1 31207283 ref XP_312608.1 ENSMANGP0000014785 (Anopheles ...)	26	80
g1 129372 gb P10361 P53_RAT Cellular tumor antigen p53 (Tum...	25	144
g1 7259331 dbj BA092786.1 p53 (Macaca fuscata)	25	144
g1 693787 gb AA031269.1 tumor suppressor (Canis familiaris)	25	144
g1 8400738 ref NP_000537.2 tumor protein p53 (Homo sapiens...	25	144
g1 495056 db AA034426.1 AF071574.1 tumor suppressor protei...	25	144
g1 1709531 gb P51664 P53_SHEEP Cellular tumor antigen p53 (...)	25	144
g1 129369 sp P04637 P53_HUMAN Cellular tumor antigen p53 (T...	25	144
g1 1836145 db AA046899.1 sequence-specific transcription f...	25	144
g1 11321107 gb AA034052.1 p53 tumor suppressor (Rattus nor...	25	144
g1 16266760 dbj BA069569.1 p53 (Meriones unguiculatus)	25	144
g1 21730310 pdb 1GZHC Chain C, Crystal Structure Of The Br...	25	144
g1 6755881 ref NP_035770.1 transformation related protein ...	25	144
g1 200201 gb AA039882.1 p53	25	144
g1 1154648 emb CA062905.1 p53 [Equus caballus]	25	144
g1 2811079 sp O12946 P53_PUMR Cellular tumor antigen p53 (...)	25	144
g1 1171969 sp P41685 P53_PELCA Cellular tumor antigen p53 (...)	25	144
g1 1000577 gb AA042022.1 p53 [Canis familiaris]	25	144
g1 975651 emb CA02450.1 p53 [Callionymus lyra]	25	144
g1 20900490 ref XP_128695.1 similar to transformation rela...	25	144
g1 8698976 gb AA78535.1 AF223795.1 tumor suppressor p53 (On...	25	144

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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g1.1729419[dbj] BAA08629.1	p53 gene product (Bos primigenius)	25	144	
g1.473133[dbj] AAC08535.1	AF151521.1 tumor suppressor prote...	25	144	
g1.1072019[dbj] Q99678.P3	BARBU Cellular tumor antigen p53 ...	25	144	
g1.223827[dbj] P07197A	antigen p53, tumor	25	144	
g1.1134459[dbj] emb CAC1147.1	transformation related protein ...	25	144	
g1.18859503[ref NP_571402.1	tumor protein p53; tumor suppr...	25	144	
g1.1072018[dbj] Q99678.P3	Pig Cellular tumor antigen p53 (T...	25	144	
g1.12829194[dbj] AAC42225.1	tumor suppressor ortholog [Xiphop...	25	144	
g1.4996630[dbj] BAA78379.1	p53 [Canis familiaris]	25	144	
g1.13591878[ref NP_112281.1	tumor protein p53; tumor prote...	25	144	
g1.159374[dbj] P07193.P3	XENLA Cellular tumor antigen p53 (T...	25	144	
g1.506443[dbj] emb CAA42635.1	p53 transformation suppressor (Ho...	25	144	
g1.35353744[dbj] AAC42225.1	p53 protein (Canis familiaris)	25	144	
g1.12897872[dbj] AAF66533.1	tumor suppressor (Equus caballus)	25	144	
g1.12897872[dbj] AAF66533.1	tumor suppressor p53 (Mus musculus)	25	144	
g1.18597872[dbj] AAF66533.1	transformation related protein 5...	25	144	
g1.12897872[dbj] AAF66533.1	tumor suppressor p53 (On...	25	144	
g1.4959056[dbj] AAC42225.1	AF071573.1 tumor suppressor prote...	25	144	
g1.6641071[dbj] AAF66533.1	AF124298.1 p53 protein (Sus scrofa)	25	144	
g1.153571[dbj] emb CAA25323.1	p53 (Mus musculus)	25	144	
g1.18997097[dbj] AAC42225.1	AF75081.1 p53 (Delphinapterus le...	25	144	
g1.14039818[dbj] AAC53397.1	AF167373.1 p53 tumor suppressor (...)	25	144	
g1.28849928[ref NP_776626.1	p53 tumor suppressor phosphop...	25	144	
g1.3024331[dbj] P56423.P3	JACPA Cellular tumor antigen p53 (...)	25	144	
g1.27813081[dbj] IYCSIA	Chain A, p53-53bp2 Complex	25	144	
g1.1642241[dbj] emb CAA25652.1	p53 (Homo sapiens)	25	144	
g1.1072019[dbj] Q99678.P3	TERMU Cellular tumor antigen p53 ...	25	144	
g1.10720197[dbj] Q99678.P3	CANPO Cellular tumor antigen p53 ...	25	144	
g1.506449[dbj] emb CAA42633.1	p53 transformation suppressor (Ho...	25	144	
g1.1293681[dbj] P10360.P3	CHICK Cellular tumor antigen p53 (T...	25	144	
g1.11619833[dbj] AAB16961.1	p53 [Canis familiaris]	25	144	
g1.14719450[dbj] IYH81A	Chain A, Crystal Structure Of The No...	25	144	
g1.5064451[dbj] emb CAA42631.1	p53 transformation suppressor (Ho...	25	144	
g1.150817831[dbj] AAC08535.1	AF151521.1 tumor suppressor p53 (H...	25	144	
g1.1072019[dbj] Q99678.P3	MARMO Cellular tumor antigen p53 ...	25	144	
g1.11235551[dbj] AAC42052.1	p53 [Xiphophorus maculatus]	25	144	
g1.506443[dbj] emb CAA42630.1	p53 transformation suppressor (Ho...	25	144	
g1.21730308[dbj] IYH81A	Chain A, Crystal Structure Of The Br...	25	144	
g1.1398141[dbj] AAB61211.1	p53 antigen	25	144	
g1.12842741[dbj] Q99678.P3	BARBT Cellular tumor antigen p53 (...)	25	144	
g1.1735089[dbj] AAB93932.1	Cellular phosphoprotein p53	25	144	
g1.1398161[dbj] AAC42631.1	p53 antigen	25	144	
g1.10720193[dbj] Q99678.P3	XIPMA Cellular tumor antigen p53 ...	25	144	
g1.506441[dbj] emb CAA42629.1	p53 transformation suppressor (Ho...	25	144	
g1.60936391[dbj] Q99678.P3	CANFA Cellular tumor antigen p53 ...	25	144	
g1.10720192[dbj] Q99678.P3	ICRPU Cellular tumor antigen p53 ...	25	144	
g1.11663021[dbj] AAC37335.1	p53 [Canis familiaris]	25	144	
g1.4815351[dbj] S38824	cellular tumor antigen p53, minor spl...	25	144	
g1.386994[dbj] AAC59947.1	phosphoprotein p53 (Homo sapiens)	25	144	
g1.545102[dbj] AAC60746.1	p53 [Xenopus laevis]	25	144	
g1.10720191[dbj] Q99678.P3	XIPME Cellular tumor antigen p53 ...	25	144	

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi

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g1.20151154[dbj] IYKZYA	Chain A, Crystal Structure Of The 53...	25	144	
g1.3024331[dbj] P56424.P3	MARMO Cellular tumor antigen p53 ...	25	144	
g1.1130770[dbj] IYH81A	Chain A, p53 Core Domain In Complex W...	25	144	
g1.1938365[dbj] AAB8059.1	mutant p53 [Rattus norvegicus]	25	144	
g1.506439[dbj] emb CAA42628.1	p53 transformation suppressor (Ho...	25	144	
g1.129367[dbj] P13461.P3	CEPKE Cellular tumor antigen p53 (T...	25	144	
g1.506451[dbj] emb CAA42644.1	p53 transformation suppressor (Ho...	25	144	
g1.129377[dbj] P02340.P3	MCUSE Cellular tumor antigen p53 (T...	25	144	
g1.129373[dbj] P50351.P3	ONCXY Cellular tumor antigen p53 (T...	25	144	
g1.468314[dbj] emb CAA42672.1	p53 [Xenopus laevis]	25	144	
g1.29468129[dbj] AAC085406.1	AF368873.1 tumor suppressor p53 (...)	25	144	
g1.4859056[dbj] AAC42225.1	AF071572.1 tumor suppressor prote...	25	144	
g1.128348179[dbj] BAC37729.1	unnamed protein product (Mus mu...	25	144	
g1.5755281[dbj] BAA0327.1	p53 protein (Felis catus)	25	144	
g1.12833362[dbj] Q99678.P3	EQUNS Cellular tumor antigen p53 (...)	25	144	
g1.1282672[dbj] P19692.P3	HORSE Cellular tumor antigen p53 (...)	25	144	
g1.12842672[dbj] Q99678.P3	SPBSE Cellular tumor antigen p53 (...)	25	144	
g1.5064351[dbj] emb CAA42626.1	p53 transformation suppressor (Ho...	25	144	
g1.20521856[dbj] BAA13377.2	KIAA0246 protein (Homo sapiens)	24	194	
g1.22779437[dbj] BAC15606.1	PELR-1 (Homo sapiens)	24	194	
g1.20149782[ref NP_619613.1	stabilin 1; stabilin-1; stabl1...	24	194	
g1.12255240[ref NP_059591.1	stabilin 1 (Homo sapiens) >g1...	24	194	
g1.12329891[dbj] BAC28684.1	unnamed protein product (Mus mu...	24	194	
g1.13656617[dbj] Q99678.P3	FBN1_PIG Fibrillin 1 precursor >g1.57...	24	260	

Alignments

Get selected sequences Select all Deselect all

>g1.121355617[ref|NP_651115.1] CG10873-PA [Drosophila melanogaster]
 g1.172111769[dbj] AAF40428.1 AF224713.1 transcription factor p53 [Drosophila melano
 g1.17381624[dbj] AAF61572.1 AF244918.1 p53 tumor suppressor-like protein [Drosophi
 g1.18272608[dbj] AAF74277.1 AF250918.1 transcription factor [Drosophila melanogast
 g1.84331761[dbj] AAF75270.1 AF263722.1 transcription factor p53 [Drosophila melano
 g1.107267101[dbj] AAF56087.2 CG10873-PA [Drosophila melanogaster]
 g1.17861528[dbj] AAF39241.1 GH11591P [Drosophila melanogaster]
 g1.18032162[dbj] AAF56639.1 AF192555.1 p53-like regulator of apoptosis and cell cyc
 Length = 385

Score = 28.6 bits (60), Expect = 10
 Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 2 VOTCPKMD 9
 +CTCPKMD
 Sbjct: 260 ICTCPKMD 267

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi

7/10/2003

>gi|25009887|gb|AAJ71112.1| AT28346p [Drosophila melanogaster]
Length = 519

Score = 28.6 bits (60), Expect = 10
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 2 VCTCPKRD 9
+CTCPKRD

Subject: 394 ICTCPKRD 401

>gi|31207283|ref|XP_312608.1| ENSANGP0000014785 [Anopheles gambiae]
gi|21295812|gb|EA07957.1| ENSANGP0000014785 [Anopheles gambiae str. PEST]
Length = 338

Score = 25.7 bits (53), Expect = 80
Identities = 6/8 (75%), Positives = 8/8 (100%)

Query: 2 VCTCPKRD 9
+CTCPKRD

Subject: 310 ICTCPKRD 317

>gi|129372|gb|P10361.P3.PAT Cellular tumor antigen p53 (Tumor suppressor p53)
gi|92070|ref|S02192 cellular tumor antigen p53 - rat
gi|56829|emb|CAA31457.1| nuclear protein p53 (AA 1 - 391) [Rattus norvegicus]
Length = 391

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTPKRD 9
RVC CP RD

Subject: 271 RVCACPRGD 279

>gi|7259331|dbj|BAA92786.1| p53 [Macaca fuscata]
Length = 181

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTPKRD 9
RVC CP RD

Subject: 148 RVCACPRGD 156

>gi|693787|gb|AA31269.1| tumour suppressor [Canis familiaris]
Length = 32

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 1 RVCNCPKRD 9
RVC CP RD
Subject: 4 RVCACPRGD 12

>gi|8400738|ref|NP_000537.2| tumor protein p53 [Homo sapiens]
gi|625300|ref|DNR03 cellular tumor antigen p53 [validated] - human
gi|35214|emb|CAA38095.1| protein p53 [Homo sapiens]
gi|506437|emb|CAA2627.1| p53 transformation suppressor [Homo sapiens]
gi|3041867|gb|AAC12971.1| p53 [Homo sapiens]
gi|4732147|gb|AAD28628.1|AF136271.1 tumor suppressor protein p53 [Homo sapiens]
gi|11066970|gb|AA628785.1|AF307851.1 p53 protein [Homo sapiens]
Length = 393

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCNCPKRD 9
RVC CP RD

Subject: 273 RVCACPRGD 281

>gi|495058|gb|AAD34216.1|AF071574.1 tumor suppressor protein p53 [oncorhynchus]
Length = 265

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCNCPKRD 9
RVC CP RD

Subject: 252 RVCACPRGD 260

>gi|1209531|gb|P51664.P3.SHEEP Cellular tumor antigen p53 (Tumor suppressor p53)
gi|602357|emb|CAA57349.1| p53 [Ovis aries]
Length = 382

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCNCPKRD 9
RVC CP RD

Subject: 262 RVCACPRGD 270

>gi|129369|gb|P04637.P3.HUMAN Cellular tumor antigen p53 (Tumor suppressor p53)
p53 (Antigen NY-CO-13)
gi|35210|emb|CAA26306.1| p53 tumor antigen (aa 1-7) [Homo sapiens]
gi|189476|gb|AA59988.1| phosphoprotein p53
gi|7595312|gb|AA64408.1|AF192514.1 tumor suppressor protein p53 [Expression vect]
Length = 393

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 273 RVCACPGRD 281

>gi|1836145|gb|AAB46899.1| sequence-specific transcription factor [Equidae]
Length = 263

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 224 RVCACPGRD 232

>gi|11321107|gb|AA034052.1| p53 tumor suppressor [Rattus norvegicus]
Length = 53

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 12 RVCACPGRD 20

>gi|1626760|dbj|BAB69969.1| p53 [Meriones unguiculatus]
Length = 390

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 271 RVCACPGRD 279

>gi|21730310|pdb|1GZB|C 5 Chain C, Crystal Structure Of The Bcr1 Domains Of Hum
To The p53 Tumor Suppressor
Length = 198

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 179 RVCACPGRD 187

>gi|6755881|ref|NP_035770.1| 5 transformation related protein 53 [Mus musculus]
gi|53576|emb|CAA25625.1| 5 p53 polypeptide (aa 1-390) [Mus musculus]
gi|871421|emb|CAA25420.1| 5 cellular tumour antigen p53 [Mus musculus]
Length = 390

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 270 RVCACPGRD 278

>gi|200201|gb|AAA39882.1| 5 p53
Length = 390

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 270 RVCACPGRD 278

>gi|1154648|emb|CAA62905.1| p53 [Equus caballus]
Length = 196

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 140 RVCACPGRD 148

>gi|2811079|sp|O12946|p53_PLAFE Cellular tumor antigen p53 (Tumor suppressor p53;
gi|1922902|emb|CA70123.1| p53 [Platichthys flesus]
Length = 366

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 248 RVCACPGRD 256

>gi|1171969|sp|P41685|p53_FELCA Cellular tumor antigen p53 (Tumor suppressor p53;
gi|538225|dbj|BA05653.1| p53 [Felis catus]
Length = 386

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCNCPKRD 9
RVC CP RD
Subject: 266 RVCACPGRD 274

>gi|1000577|gb|AA042022.1| p53 [canis familiaris]
Length = 276

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCNCPKRD 9
RVC CP RD
Subject: 237 RVCACPGRD 245

>gi|975651|emb|CAA62450.1| p53 [Callionymus lyra]
Length = 45

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCNCPKRD 9
RVC CP RD
Subject: 37 RVCACPGRD 45

>gi|20900490|ref|XP_128695.1| similar to transformation related protein 53 [M.
Length = 151

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCNCPKRD 9
RVC CP RD
Subject: 114 RVCACPGRD 122

>gi|8698976|gb|AA078535.1|AF223795.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8698976|gb|AA078535.1|AF223795.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8698980|gb|AA078537.1|AF223797.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8698982|gb|AA078538.1|AF223798.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8698984|gb|AA078539.1|AF223799.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8698986|gb|AA078540.1|AF223800.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8698988|gb|AA078541.1|AF223801.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8698990|gb|AA078542.1|AF223802.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8698992|gb|AA078543.1|AF223803.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8698994|gb|AA078544.1|AF223804.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8698996|gb|AA078545.1|AF223805.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8698998|gb|AA078546.1|AF223806.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8699000|gb|AA078547.1|AF223807.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8699002|gb|AA078548.1|AF223808.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8699004|gb|AA078549.1|AF223809.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8699006|gb|AA078550.1|AF223810.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8699008|gb|AA078551.1|AF223811.1 tumor suppressor p53 [Oncothynchus tshawytscha]

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

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gi|8699010|gb|AA078552.1|AF223812.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8699012|gb|AA078553.1|AF223813.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8699014|gb|AA078554.1|AF223814.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8699016|gb|AA078555.1|AF223815.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8699018|gb|AA078556.1|AF223816.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8699020|gb|AA078557.1|AF223817.1 tumor suppressor p53 [Oncothynchus tshawytscha]
gi|8699022|gb|AA078558.1|AF223818.1 tumor suppressor p53 [Oncothynchus tshawytscha]

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCNCPKRD 9
RVC CP RD
Subject: 42 RVCACPGRD 50

>gi|1729419|dbj|BAA08629.1| p53 gene product [Bos primigenius]
Length = 374

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCNCPKRD 9
RVC CP RD
Subject: 254 RVCACPGRD 262

>gi|4731632|gb|AA028535.1|AF135121.1 tumor suppressor protein p53 [Homo sapiens]
Length = 393

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCNCPKRD 9
RVC CP RD
Subject: 273 RVCACPGRD 281

>gi|10720195|gb|Q9W678|P53_BABBU Cellular tumor antigen p53 (Tumor suppressor p53)
gi|4959050|gb|AA034212.1|AF071570.1 tumor suppressor protein p53 [Barbus barbus]

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCNCPKRD 9
RVC CP RD
Subject: 237 RVCACPGRD 245

>gi|223827|ref|U001197A antigen p53, tumor
Length = 390
Score = 24.8 bits (51), Expect = 144

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 270 RVCACPRGD 278

>gi|11342599|emb|CAC17147.1| **1** transformation related protein 53 [Mus musculus]
Length = 307

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 270 RVCACPRGD 278

>gi|18859503|ref|NP_571402.1| **1** tumor protein p53; tumor suppressor homolog p53;
antigen p53 [Danio rerio]
gi|2829677|sp|P79734|p53_BRAE Cellular tumor antigen p53 (Tumor suppressor p53)
gi|1778019|gb|AA040617.1| **1** tumor suppressor p53 [Danio rerio]
Length = 373

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 241 RVCACPRGD 249

>gi|10720186|sp|Q9TUN2|P53_PIG Cellular tumor antigen p53 (Tumor suppressor p53)
gi|6165623|gb|AA04620.1|AF08067.1 tumor suppressor p53 [Sus scrofa]
Length = 386

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 266 RVCACPRGD 274

>gi|2829194|gb|AAC26190.1| tumor suppressor ortholog [Xiphophorus maculatus]
Length = 153

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 47 RVCACPRGD 55

>gi|4996230|dbj|BA078379.1| p53 [Canis familiaris]
Length = 381

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 281 RVCACPRGD 269

>gi|13591878|ref|NP_112251.1| **1** tumor protein p53; tumor protein p53 (Li-Fraumeni
notregicus)
gi|205952|gb|AA041788.1| **1** tumor suppressor
Length = 391

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 271 RVCACPRGD 279

>gi|129374|sp|P07193|P53_XENLA Cellular tumor antigen p53 (Tumor suppressor p53)
gi|85718|pir|A29376 Cellular tumor antigen p53 - African clawed frog
gi|64962|emb|CA28821.1 ORF (AA 1-363) [Xenopus laevis]
gi|214640|gb|AA049923.1 p53 protein homologue; putative
Length = 363

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 248 RVCACPRGD 256

>gi|506453|emb|CAA2635.1| **1** p53 transformation suppressor [Homo sapiens]
Length = 393

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 273 RVCACPRGD 281

>gi|5353744|gb|AAD42225.1| p53 protein [Canis familiaris]
Length = 246

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 156 RVCACPGRD 164

>gi|1389675|gb|AA018936.1| tumor-suppressor [Equus caballus]
Length = 205

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 149 RVCACPGRD 157

>gi|2961247|gb|AAC05704.1| tumor suppressor p53 [Mus musculus]
Length = 390

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 270 RVCACPGRD 278

>gi|15375072|gb|AAK94783.1| transformation related protein 53 [Mus musculus]
Length = 391

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 270 RVCACPGRD 278

>gi|8698972|gb|AAF78533.1|AF223793.1 tumor suppressor p53 [Oncomorphus mykiss]
gi|8698974|gb|AAF78534.1|AF223794.1 tumor suppressor p53 [Oncomorphus mykiss]
Length = 146

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 42 RVCACPGRD 50

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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>gi|28975327|gb|AA060156.1| tumor suppressor p53, p53as [Mus musculus]
Length = 381

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 270 RVCACPGRD 278

>gi|4959056|gb|AA034215.1|AF071573.1 tumor suppressor protein p53 [Oncomorphus]
Length = 265

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 252 RVCACPGRD 260

>gi|6641071|gb|AA028891.1|AF124298.1 p53 protein [Sus scrofa]
Length = 387

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 262 RVCACPGRD 270

>gi|53571|emb|CAA25323.1| p53 [Mus musculus]
Length = 389

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 269 RVCACPGRD 277

>gi|18997097|gb|AA083290.1|AF475081.1 p53 [Delphinapterus leucas]
Length = 387

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCTCPKRD 9
RVC CP RD
Sbjct: 267 RVCACPGRD 275

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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>gi|14039818|gb|AAK53397.1|AF367373.1 p53 tumor suppressor [Mus musculus]
Length = 207

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 148 RVCACPFGRD 156

>gi|28849929|ref|NP_776626.1| p53 tumor suppressor phosphoprotein (Bos taurus)
gi|2499426|sp|Q29628|P53_BOVIN Cellular tumor antigen p53 (Tumor suppressor p53)
gi|1083096|p|I|S51648 cellular tumor antigen p53 - bovine
gi|602333|emb|CAA57348.1| p53 [Bos taurus]
gi|1916676|gb|AAK51214.1| 53 kDa phosphoprotein [Bos indicus]
Length = 386

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 266 RVCACPFGRD 274

>gi|3024331|sp|P56423|P53_MACPA Cellular tumor antigen p53 (Tumor suppressor p53)
gi|2689467|gb|AAK51535.1| P53 [Macaca fascicularis]
Length = 393

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 273 RVCACPFGRD 281

>gi|2781308|pdb|1YCS|A Chain A, p53-53bp2 Complex
Length = 199

Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 180 RVCACPFGRD 188

>gi|642241|emb|CAA25652.1| p53 [Homo sapiens]
Length = 293

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi

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Score = 24.8 bits (51), Expect = 144
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 RVCCTCPKRD 9
RVC CP RD
Sbjct: 173 RVCACPFGRD 181

Get selected sequences Selected all Deselect all

Database: All non-redundant Genbank CDS
translations+PDB+SwissProt+PIR+PP
Posted date: Jul 10, 2003 1:49 AM
Number of letters in database: 474,244,320
Number of sequences in database: 1,477,204

Lambda	K	H
0.357	0.295	2.13
Gapped	K	H
Lambda	0.294	0.110
	0.110	0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of Hits to DB: 7,701,129
Number of Sequences: 1477204
Number of extensions: 39535
Number of successful extensions: 1949
Number of sequences better than 20000.0 without gapping: 1769
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
length of query: 9
length of database: 474,244,320
effective HSP length: 0
effective length of query: 9
effective length of database: 474,244,320
effective search space: 4268198880
effective search space used: 4268198880
T: 11
A: 40
X1: 14 (7.2 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 35 (19.8 bits)
S2: 35 (18.0 bits)

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi

7/10/2003

NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jiongchi Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

RID: 1057870092-013883-18202

Query= SEQID30
(9 letters)

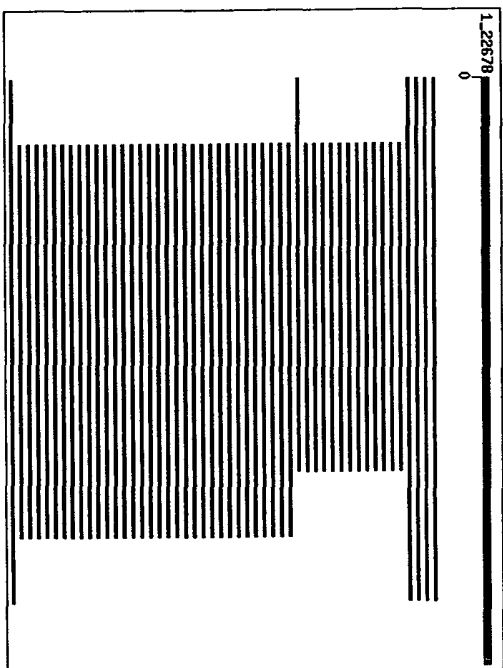
Database: All non-redundant Genbank CDS
translations+PDB+SwissProt+PIR+PIF
1,477,204 sequences; 474,244,320 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQ](#)

[Taxonomy reports](#)

Distribution of 125 Blast Hits on the Query Sequence

[Mouse-over to show define and scores. Click to show alignments](#)



Related Structures

Sequences producing significant alignments:

	Score	E
	(bits)	Value
g1 21355617 ref NP_651115.1 CG10873-PA [Drosophila melanogaster]	32	1.3
g1 25009887 gb AA71112.1 AT28346P [Drosophila melanogaster]	32	1.3
g1 31207283 ref NP_312608.1 ENSMUSGP0000014785 [Anopheles ...]	29	10
g1 18150104 db BAAB81667.1 insulin receptor [Paralichthys ...]	24	194
g1 13626617 sp Q9TV36 FBN1_PIG Fibrillin 1 precursor >g1 57...	24	260
g1 3588648 gb AAC62317.1 mutant fibrillin-1 [Mus musculus]	24	260
g1 642072 gb AA61825.1 fibrillin-1	24	260
g1 13929178 ref NP_114013.1 fibrillin-1 [Rattus norvegicus...]	24	260
g1 24430141 ref NP_000129.2 fibrillin 1 [Homo sapiens]	24	260
g1 7459677 gb AA7221 fibrillin 1 precursor - human (fragm...	24	260
g1 2494284 sp O61554 FBN1_MOUSE Fibrillin 1 precursor >g1 1...	24	260
g1 6679759 ref NP_032019.1 fibrillin 1; tight skin [Mus mu...	24	260
g1 27806637 ref NP_776478.1 fibrillin 1 [Bos taurus] >g1 1...	24	260
g1 28487571 ref XP_192917.2 fibrillin 1 [Mus musculus]	24	260
g1 544279 sp P35555 FBN1_HUMAN Fibrillin 1 precursor >g1 30...	24	260
g1 1335064 emb CA45118.1 fibrillin [Homo sapiens]	24	260
g1 1729929 sp P80424 DVT_HIRME Leech-derived cryptase inhib...	24	349
g1 16506777 gb AA23943.1 AF425233.5 putative aldehyde dehy...	23	628
g1 21229579 ref NP_635496.1 chlozoacetaldehyde dehydrogena...	23	628
g1 17988030 ref NP_540664.1 ALDEHYDE DEHYDROGENASE [Brucei...	23	628
g1 9652162 gb AAFP91420.1 AF277380.1 aldehyde dehydrogenase ...	23	628
g1 23015854 ref U2P_00055619.1 hypothetical protein [Magnet...	23	628

g1 15597180 ref NP_250674.1	probable aldehyde dehydrogenase...	23	628
g1 28867956 ref NP_790575.1	aldehyde dehydrogenase family ...	23	628
g1 23308979 ref NP_601988.2	NAD-dependent aldehyde dehydro...	23	628
g1 23099989 ref NP_693455.1	aldehyde dehydrogenase (locano...	23	628
g1 2660726 ref NP_230467.1	aldehyde dehydrogenase (vibrio...	23	628
g1 2660726 ref NP_230467.1	aldehyde dehydrogenase (vibrio...	23	628
g1 23062064 ref NP_00086869.1	NAD-dependent chloroacetaldehyde...	23	628
g1 15613244 ref NP_21547.1	hypothetical protein [Pseudo...	23	628
g1 15593281 gb AA02234.1 AF414083.5	aldehyde dehydrogenase (Bacill...	23	628
g1 30065134 ref NP_839305.1	putative truncated ald...	23	628
g1 1475541 ref NP_107705.1	aldehyde dehydrogenase (Mesorh...	23	628
g1 26989399 ref NP_744824.1	aldehyde dehydrogenase family ...	23	628
g1 28831719 ref NP_828351.1	putative aldehyde dehydrogenase...	23	628
g1 17936107 ref NP_512897.1	aldehyde dehydrogenase (Agrob...	23	628
g1 15283977 gb AA28545.2	putative aldehyde dehydrogenase...	23	628
g1 15966104 ref NP_386457.1	PROBABLY ALDEHYDE DEHYDROGENAS...	23	628
g1 2466995 ref NP_765672.1	glycine betaine aldehyde dehyd...	23	628
g1 15889500 ref NP_355181.1	AGR_C_404ip (Agrobacterium tum...	23	628
g1 2431958 ref NP_70001.1	aldehyde dehydrogenase (Shewan...	23	628
g1 15152093 gb AA14969.1 AF418982.6	aldehyde dehydrogenase B (lact...	23	628
g1 13286801 gb AAC79659.1	NAD+ dependent acetaldehyde dehy...	23	628
g1 14519175 gb BAA75508.1	aldehyde dehydrogenase (Petroleu...	23	628
g1 27379895 ref NP_771424.1	aldehyde dehydrogenase (Pseud...	23	628
g1 23469955 ref NP_00125289.1	hypothetical protein [Pseudo...	23	628
g1 21219683 ref NP_625464.1	aldehyde dehydrogenase (Strept...	23	628
g1 13825005 gb AA09566.1 AF67720.1	lipoprotein receptor...	23	628
g1 23008821 ref NP_00049754.1	hypothetical protein [Mann...	23	628
g1 15076881 gb AA82977.1	NAD+-dependent aldehyde dehydro...	23	628
g1 15641821 ref NP_231453.1	aldehyde dehydrogenase (Vibrio...	23	628
g1 15607389 ref NP_214972.1	hypothetical protein RV0458 (M...	23	628
g1 2502131 ref NP_739235.1	putative aldehyde dehydrogenase...	23	628
g1 26606001 gb BAA24014.1	aldehyde dehydrogenase (Altecom...	23	628
g1 26502020 ref NP_756270.1	aldehyde dehydrogenase B [Psc...	23	628
g1 32031931 ref NP_00137465.1	hypothetical protein [Pseudo...	23	628
g1 47586861 ref NP_002323.1	low density lipoprotein-related...	23	628
g1 15808007 ref NP_285671.1	aldehyde dehydrogenase (Pdenoc...	23	628
g1 16127810 ref NP_422374.1	aldehyde dehydrogenase B (cau...	23	628
g1 26987283 ref NP_742708.1	aldehyde dehydrogenase family ...	23	628
g1 16131459 ref NP_418045.1	aldehyde dehydrogenase B (lact...	23	628
g1 66787201 ref NP_032538.1	low density lipoprotein recepto...	23	628
g1 28898477 ref NP_798082.1	aldehyde dehydrogenase (Vibrio...	23	628
g1 1185011 gb E23240 DHAL_VIBCH	aldehyde dehydrogenase >g1 7...	23	628
g1 27367274 ref NP_762801.1	NAD-dependent aldehyde dehydro...	23	628
g1 15604128 ref NP_280167.1	aldehyde dehydrogenase B (lact...	23	628
g1 32042073 ref NP_00139656.1	hypothetical protein [Pseudo...	23	628
g1 11683071 gb P463681 DHA2_ALCEU	Acetaldehyde dehydrogenase...	23	628
g1 23501111 ref NP_697238.1	aldehyde dehydrogenase family ...	23	628
g1 16762629 ref NP_458246.1	aldehyde dehydrogenase B (sal...	23	628
g1 16766965 ref NP_462580.1	aldehyde dehydrogenase B (lact...	23	628
g1 27881810 gb BAH43675.1	Similar to low density lipoprote...	23	628
g1 17088644 gb P981571 LRRP1_CHICK	Low-density lipoprotein rec...	23	628
g1 15395217 ref NP_252711.1	probable aldehyde dehydrogenase...	23	628
g1 32042073 ref NP_00139658.1	hypothetical protein [Pseudo...	23	628
g1 11684051 gb P376851 ALDH_ECOLI	Aldehyde dehydrogenase B (l...	23	628
g1 22985941 ref NP_00031048.1	hypothetical protein [Burkho...	23	628
g1 22986033 ref NP_00031138.1	hypothetical protein [Burkho...	23	628
g1 21240903 ref NP_604045.1	chloroacetaldehyde dehydrogena...	23	628
g1 21020471 ref NP_00088576.1	hypothetical protein [Azotob...	23	628

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7/10/2003

g1 2660722 gb AA313641.1	chloroacetaldehyde dehydrogenase ...	23	628
g1 19936655 gb BAH1888.1	aldehyde dehydrogenase 1 (Acinet...	23	628
g1 15825096 gb AA09567.1	lipoprotein receptor-related pro...	23	628
g1 115547847 ref NP_521249.1	FOUNTAIN NAD+ DEPENDENT ACETALD...	23	628
g1 22963184 ref NP_00010790.1	hypothetical protein [Rhodop...	23	628
g1 12298082 ref NP_00025793.1	hypothetical protein [Ralsto...	23	628
g1 23867780 gb BAC21014.1	claudin4L2 [Xenopus laevis]	22	843
g1 13569662 emb CND2165.1	putative dehydrogenase subunit ...	22	843
g1 13848262 gb BMB27889.1	unnamed protein product [Mus mu...	22	843
g1 125150357 ref NP_741619.1	Pro-collagen domains family me...	22	843
g1 15605825 ref NP_213302.1	hypothetical protein [Aquifex ...	22	843
g1 1109335 gb P21783 NOTC_XENLA	Neurogenic locus notch prot...	22	1131
g1 18859115 ref NP_571516.1	notch homolog 1a; neurogenic 1...	22	1131
g1 2767874 ref NP_228125.1	similar to 40kDa ribosomal pro...	22	1131
g1 104232 gb P135844	Xoroc protein - African clawed frog	22	1131
g1 1293721 gb P1361 P53_RAT	Cellular tumor antigen p53 (Tum...	21	1518
g1 7259331 gb BAA92786.1	p53 (Macaca fasciata)	21	1518
g1 189479 gb AA59989.1	p53 cellular tumor antigen	21	1518
g1 1693787 gb BAA31269.1	tumor suppressor [Canis familiaris]	21	1518

Alignments

Get selected sequences:	Select all	Deselect all
-------------------------	------------	--------------

>g1|23355617|ref|NP_651115.1| CG10873-PA [Drosophila melanogaster]
 g1|2111767|gb|AA40427.1|AF224713.1 transcription factor p53 [Drosophila melano]
 g1|2111769|gb|AA40428.1|AF224714.1 transcription factor p53 [Drosophila melano]
 g1|2381624|gb|AA61572.1|AF244918.1 p53 tumor suppressor-like protein [Drosophi
 g1|8272608|gb|AA74277.1|AF250918.1 transcription factor [Drosophila melanogaster]
 g1|8453176|gb|AA75270.1|AF263722.1 transcription factor p53 [Drosophila melano
 g1|10726710|gb|AA756087.2| CG10873-PA [Drosophila melanogaster]
 g1|17861528|gb|AA139241.1| GH11591p [Drosophila melanogaster]
 g1|18032162|gb|AA156639.1|AF192555.1 p53-like regulator of apoptosis and cell cyc
 melanogaster]
 Length = 385

Score = 31.6 bits (67), Expect = 1.3
 Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 1 KYCCPKRD 9
 K-KCCPKRD
 Sbjct: 259 KYCCPKRD 267

>g1|25098887|gb|AA71112.1| AT78346p [Drosophila melanogaster]
 Length = 519

Score = 31.6 bits (67), Expect = 1.3
 Identities = 8/9 (88%), Positives = 9/9 (100%)

http://www.ncbi.nlm.nih.gov/biast/Blast.cgi

7/10/2003

Query: 1 KVCTCPKRD 9
K+CTCPKRD
Sbjct: 393 KICCTCPKRD 401

[>gi|31207283|ref|XP_312608.1| ENSANGP00000014785 [Anopheles gambiae]
gi|21295812|gb|EA07957.1| ENSANGP00000014785 [Anopheles gambiae str. pcr1]
Length = 338

Score = 28.6 bits (60), Expect = 10
Identities = 7/9 (77%), Positives = 9/9 (100%)

Query: 1 KVCTCPKRD 9
K+C+CTCPKRD
Sbjct: 309 KICCTCPKRD 317

[>gi|18150104|db|BAB3667.1| insulin receptor [Paralichthys olivaceus]
Length = 1369

Score = 24.4 bits (50), Expect = 194
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 1 KVCTCPKRD 9
KVC CPK D
Sbjct: 705 KVCACPKRD 713

[>gi|13626617|sp|Q9TV36|FBN1-PIG Fibrillin 1 precursor
gi|5739075|gb|AA050328.1|AF073800.1 fibrillin-1 precursor [Sus scrofa]
Length = 2872

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7
VCTCPK
Sbjct: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 100 CTCP 103

[>gi|3688648|gb|AAC62317.1| mutant fibrillin-1 [Mus musculus]
Length = 3857

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 2 VCTCPK 7
VCTCPK
Sbjct: 1775 VCTCPK 1780

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7
VCTCPK
Sbjct: 791 VCTCPK 796

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 100 CTCP 103

[>gi|642072|gb|AA61825.1| fibrillin-1
Length = 1095

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7
VCTCPK
Sbjct: 766 VCTCPK 771

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 75 CTCP 78

[>gi|13929178|ref|NP_114013.1| fibrillin-1 [Rattus norvegicus]
gi|4959650|db|AA034438.1| fibrillin-1 [Rattus norvegicus]
Length = 2872

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7
VCTCPK
Sbjct: 790 VCTCPK 795

Score = 18.0 bits (35), Expect = 15950

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6

Subject: 100 CTCP 103

>gi|24430141|ref|NP_000129.2| **1** fibrillin 1 (Homo sapiens)
Length = 2871

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7

Subject: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6

Subject: 100 CTCP 103

>gi|7459676|ref|AA7221 fibrillin 1 precursor - human (fragment)
Length = 3002

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7

Subject: 920 VCTCPK 925

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6

Subject: 231 CTCP 234

>gi|2494284|ref|Q61554|PBN1_MOUSE **1** Fibrillin 1 precursor
gi|10833181|ref|A55624 fibrillin-1 precursor - mouse
gi|575510|ref|AA56840.1 **1** fibrillin
Length = 2871

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

VCTCPK
Subject: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6

Subject: 100 CTCP 103

>gi|6679759|ref|NP_032019.1| **1** fibrillin 1, tight skin [Mus musculus]
gi|726324|ref|AA64217.1| **1** fibrillin-1
Length = 2873

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7

Subject: 791 VCTCPK 796

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6

Subject: 100 CTCP 103

>gi|27806637|ref|NP_776478.1| **1** fibrillin 1 (Bos taurus)
gi|1706768|ref|P98133|PBN1_BOVIN Fibrillin 1 precursor (WP340)
gi|1083029|ref|A55567 fibrillin I - bovine
gi|508428|ref|AA74122.1| **1** putative
Length = 2871

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7

Subject: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6

Subject: 100 CTCP 103

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

>gi|28487571|ref|XP_192917.2| **1** fibrillin 1 [Mus musculus]
Length = 2873

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7
VCTCPK
Sbjct: 791 VCTCPK 796

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 100 CTCP 103

>gi|544279|sp|E35555|FBN1_HUMAN **1** Fibrillin 1 precursor
gi|306746|gb|AA02036.1| **1** fibrillin
gi|455558|gb|AA02036.1| fibrillin [human, Marfan syndrome patient, Peptide Mutan
Length = 2871

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7
VCTCPK
Sbjct: 789 VCTCPK 794

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 3 CTCP 6
CTCP
Sbjct: 100 CTCP 103

>gi|1335064|emb|CAA45118.1| **1** fibrillin [Homo sapiens]
Length = 3002

Score = 24.0 bits (49), Expect = 260
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 2 VCTCPK 7
VCTCPK
Sbjct: 920 VCTCPK 925

Score = 18.0 bits (35), Expect = 15950
Identities = 4/4 (100%), Positives = 4/4 (100%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 3 CTCP 6
CTCP
Sbjct: 231 CTCP 234

>gi|729929|sp|P80424|LDTI_HIRME leech-derived trypsin inhibitor (LDTI)
gi|7511702|db|SS0015 leech-derived trypsin inhibitor - medicinal leech
gi|3212564|db|LDTI.L **1** Chain L, Complex Of Leech-Derived Trypsin Inhibitor With
Porcine Trypsin
gi|3318723|db|JAN11 **1** Chain I, Leech-Derived Trypsin Inhibitor
gi|99917|gb|AA033769.1 master cell trypsin inhibitor, LDTI (hirudo
medicinalis=medicinal leeches, Peptide, 46 aa)
Length = 46

Score = 23.5 bits (48), Expect = 349
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 KVCCTCPK 7
KVC CPK
Sbjct: 2 KVCACPK 8

>gi|1650677|gb|AA023943.1|AF425233.5 putative aldehyde dehydrogenase [Versinia
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPK 8
VCTCP R
Sbjct: 300 VCTCPK 306

>gi|21229579|ref|NP_635496.1| chloroacetaldehyde dehydrogenase [Xanthomonas cam
campestris str. ATCC 33913]
gi|2111050|gb|AA039420.1 chloroacetaldehyde dehydrogenase [Xanthomonas campestr
campestris str. ATCC 33913]
Length = 509

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPK 8
VCTCP R
Sbjct: 303 VCTCPK 309

>gi|17988030|ref|NP_540664.1| ALDEHYDE DEHYDROGENASE [Brucella melitensis]
gi|25284280|db|AB0470 aldehyde dehydrogenase (NAD) (EC 1.2.1.3) [imported] - Br
melitensis (strain 16M)
gi|17983776|gb|AA052928.1| ALDEHYDE DEHYDROGENASE [Brucella melitensis 16M]
Length = 505

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPSR 8
VCTCP R
Sbjct: 299 VCTCPSR 305

[>gi|3652162|gb|AAE91420.1|AF277380.1] aldehyde dehydrogenase [Acetobacter vinelae]
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPSR 8
VCTCP R
Sbjct: 300 VCTCPSR 306

[>gi|23015854|ref|XP_00055619.1] hypothetical protein [Magnetospirillum magnetococcus]
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPSR 8
VCTCP R
Sbjct: 300 VCTCPSR 306

[>gi|15597180|ref|NP_250674.1] probable aldehyde dehydrogenase [Pseudomonas aeruginosa strain PA01]
gi|11350933|pir|H83396 probable aldehyde dehydrogenase PA1984 [imported] - Pseud
gi|19947985|gb|AA05372.1|AB004625.2 probable aldehyde dehydrogenase [Pseudomonas]
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPSR 8
VCTCP R
Sbjct: 300 VCTCPSR 306

[>gi|28867956|ref|NP_790575.1] aldehyde dehydrogenase family protein [Pseudomonas tomato str. DC3000]
gi|28851192|gb|AA054270.1] aldehyde dehydrogenase family protein [Pseudomonas syri]
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPSR 8
VCTCP R

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Sbjct: 300 VCTCPSR 306

[>gi|23308979|ref|NP_601988.2] NAD-dependent aldehyde dehydrogenase [Corynebacterium ATCC 13032]
gi|12125568|dbj|BAC00190.1] NAD-dependent aldehyde dehydrogenases [Corynebacterium ATCC 13032]
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPSR 8
VCTCP R
Sbjct: 301 VCTCPSR 307

[>gi|2309989|ref|NP_693455.1] aldehyde dehydrogenase [Oceanobacillus ihayensis] H78
gi|22778220|dbj|BAC14490.1] aldehyde dehydrogenase [Oceanobacillus ihayensis H78]
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPSR 8
VCTCP R
Sbjct: 300 VCTCPSR 306

[>gi|15640836|ref|NP_230467.1] aldehyde dehydrogenase [Vibrio cholerae]
gi|11251887|pir|A82276 aldehyde dehydrogenase VC0819 [imported] - Vibrio cholerae
gi|1965269|gb|AA93982.1] aldehyde dehydrogenase [Vibrio cholerae]
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPSR 8
VCTCP R
Sbjct: 335 VCTCPSR 341

[>gi|2660726|gb|AAC13644.1] NAD-dependent chloroacetaldehyde dehydrogenase [Xantho autotrophicus]
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPSR 8
VCTCP R
Sbjct: 300 VCTCPSR 306

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

>gi|23062064|ref|ZP_00086869.1| hypothetical protein [Pseudomonas fluorescens Pf]
Length = 520

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPR 8
VCTCP R
Sbjct: 314 VCTCPR 320

>gi|15613244|ref|NP_243547.1| aldehyde dehydrogenase [Bacillus halodurans]
gi|25284184|pir|A83735 aldehyde dehydrogenase aldA [imported] - Bacillus halodur
(strain C-125)
gi|1017295|db|BAB04400.1| aldehyde dehydrogenase [Bacillus halodurans]
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPR 8
VCTCP R
Sbjct: 300 VCTCPR 306

>gi|15593281|gb|AA02234.1|AF414083.5 putative truncated aldehyde dehydrogenase
pseudotuberculosis]
Length = 258

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPR 8
VCTCP R
Sbjct: 52 VCTCPR 58

>gi|30065134|ref|NP_839305.1| aldehyde dehydrogenase B [lactaldehyde dehydrogen
flexneri 2a str. 2457r]
gi|30043395|gb|AA019116.1| aldehyde dehydrogenase B [lactaldehyde dehydrogenase]
flexneri 2a str. 2457r]
Length = 542

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPR 8
VCTCP R
Sbjct: 336 VCTCPR 342

>gi|13475541|ref|NP_107105.1| aldehyde dehydrogenase [Mesorhizobium loti]
gi|14026293|db|BA552893.1| aldehyde dehydrogenase [Mesorhizobium loti]

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

Length = 505

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPR 8
VCTCP R
Sbjct: 299 VCTCPR 305

>gi|26989399|ref|NP_744824.1| aldehyde dehydrogenase family protein [Pseudomonas]
gi|24984262|db|AA08288.1|AE016463.2 aldehyde dehydrogenase family protein [Pseud]
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPR 8
VCTCP R
Sbjct: 300 VCTCPR 306

>gi|29833719|ref|NP_828353.1| putative aldehyde dehydrogenase [Streptomyces averm]
gi|29610843|db|BAC74888.1| putative aldehyde dehydrogenase [Streptomyces averm]
Length = 507

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPR 8
VCTCP R
Sbjct: 301 VCTCPR 307

>gi|17936107|ref|NP_532897.1| aldehyde dehydrogenase [Agrobacterium tumefaciens
Washington]
gi|25284266|pir|AG2849 aldehyde dehydrogenase aldA [imported] - Agrobacterium tu
(strain C58, Dupont)
gi|17740695|gb|AA043213.1| aldehyde dehydrogenase [Agrobacterium tumefaciens str.
Washington]
Length = 505

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPR 8
VCTCP R
Sbjct: 299 VCTCPR 305

>gi|15283977|gb|AA028545.2| putative aldehyde dehydrogenase [Yersinia pseudotub]
Length = 506
Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

Query: 2 VCTCPK 8
VCTCP R
Sbjct: 300 VCTCPSR 306

>gi|15966104|ref|NP_386457.1| PROBABLE ALDEHYDE DEHYDROGENASE PROTEIN [Sinorhizogium
gi|15075374|emb|CAC6930.1|
Length = 502

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPK 8
VCTCP R
Sbjct: 296 VCTCPSR 302

>gi|27469851|ref|NP_765622.1| glycine betaine aldehyde dehydrogenase gbsa [Scap]
epidermidis ATCC 122281
gi|27316534|gb|AA005709.1|AE016751.4 glycine betaine aldehyde dehydrogenase gbsa
epidermidis ATCC 122281
Length = 479

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 2 VCTCPK 8
VCTCP+R
Sbjct: 285 VCTCPSR 291

>gi|15889500|ref|NP_355181.1| AGR_C_4041p [Agrobacterium tumefaciens]
gi|252842481|db|E97626 chloroacetaldehyde dehydrogenase (AF029733) [imported] -
Agrobacterium tumefaciens (strain C58, Cereon)
gi|15157374|gb|AA87966.1| AGR_C_4041p [Agrobacterium tumefaciens str. C58 (Cereon)
Length = 540

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPK 8
VCTCP R
Sbjct: 334 VCTCPSR 340

>gi|24375958|ref|NP_720001.1| aldehyde dehydrogenase [Shewanella oneidensis MR-1]
gi|24350948|gb|AA57445.1|AE015880.4 aldehyde dehydrogenase [Shewanella oneidensis]
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPK 8
VCTCP R

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Sbjct: 300 VCTCPSR 306

>gi|24414856|ref|NP_709366.1| aldehyde dehydrogenase B (lactaldehyde dehydrogen
flexneri 2a str. 301)
gi|24054091|gb|AA45073.1|AE015370.10 aldehyde dehydrogenase B (lactaldehyde dehy
flexneri 2a str. 301)
Length = 558

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPK 8
VCTCP R
Sbjct: 352 VCTCPSR 358

>gi|16152091|gb|AA14969.1|AF18982.6 putative aldehyde dehydrogenase [Yersinia
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPK 8
VCTCP R
Sbjct: 300 VCTCPSR 306

>gi|39286801|gb|AACT9659.1| NAD+ dependent acetaldehyde dehydrogenase [Pseudomon
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPK 8
VCTCP R
Sbjct: 300 VCTCPSR 306

>gi|45191751|db|BA15508.1| aldehyde dehydrogenase [petroleum-degrading bacteri
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPK 8
VCTCP R
Sbjct: 300 VCTCPSR 306

>gi|27379895|ref|NP_771424.1| aldehyde dehydrogenase [Bradyrhizobium japonicum]
gi|27353048|db|BA50049.1| aldehyde dehydrogenase [Bradyrhizobium japonicum USDA
Length = 505

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8
VCTCP R
Sbjct: 299 VCTCPSR 305

>gi|23469955|ref|ZP_00125289.1| hypothetical protein [Pseudomonas syringae pv.]
Length = 506

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8
VCTCP R
Sbjct: 300 VCTCPSR 306

>gi|21219685|ref|NP_625464.1| aldehyde dehydrogenase [Streptomyces coelicolor A:
gi|8928070|sp|ORF26|DHAL_STRCO Probable aldehyde dehydrogenase
gi|6468426|emb|CB61386.1| aldehyde dehydrogenase [Streptomyces coelicolor A3(2)]
Length = 507

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8
VCTCP R
Sbjct: 301 VCTCPSR 307

>gi|15825005|db|AA109566.1|AF367720.1 1 lipoprotein receptor-related protein (M
Length = 4545

Score = 22.7 bits (46), Expect = 628
Identities = 7/9 (77%), Positives = 7/9 (77%), Gaps = 2/9 (22%)

Query: 2 VCTCP--KR 8
VCTCP KR
Sbjct: 4169 VCTCPNGKR 4177

Score = 18.0 bits (35), Expect = 15950
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 2 VCTCP 6
VC+CP
Sbjct: 1206 VCSCP 1210

>gi|23008217|ref|ZP_00049754.1| hypothetical protein [Magnetospirillum magnetot
Length = 260

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 22.7 bits (46), Expect = 628
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 2 VCTCPKR 8
VCTCP R
Sbjct: 54 VCTCPSR 60

Get selected sequences Select all Deselected all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Jul 10, 2003 1:49 AM
Number of letters in database: 474,244,320
Number of sequences in database: 1,477,204

Lambda K H
0.360 0.295 2.12

Gapped
Lambda K H
0.294 0.110 0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of Hits to Db: 7,726,919
Number of Sequences: 1477204
Number of extensions: 34981
Number of successful extensions: 1887
Number of sequences better than 20000.0: 100
Number of HSP's better than 20000.0 without gapping: 1713
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1887
length of query: 9
length of database: 474,244,320
effective HSP length: 0
effective length of query: 9
effective length of database: 474,244,320
effective search space: 4268198880
effective search space used: 4268198880
T: 11
A: 40

X1: 14 (7.3 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 35 (19.9 bits)
S2: 35 (18.0 bits)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

NCBI results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057871489-08294-14294

Query= SEQID31
(7 letters)

Databases: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PPF
1,477,204 sequences; 474,244,320 total letters

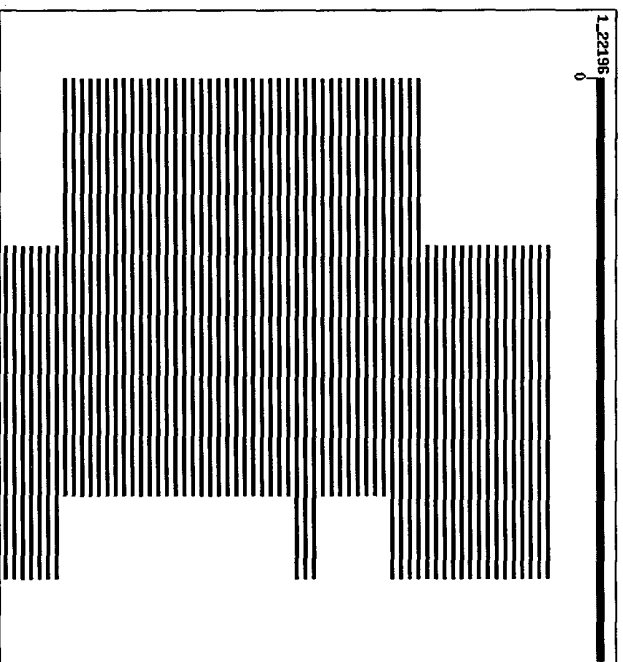
If you have any problems or questions with the results of this search
please refer to the [BLAST Page](#)

[Taxonomy Reports](#)

Distribution of 90 Blast Hits on the Query Sequence

[Mouse over to show define and scores. Click to show alignments](#)

EXHIBIT M



Sequences producing significant alignments:

	Score	E
	(bits)	Value
gi 17981441 gb AAU51006.1 AF454393.1 folliculin [Drosophila...]	21	2733
gi 23822094 sp O8SP28 PANTR_Ribonuclease_8_precursor [...]	21	2733
gi 17508299 ref NP_490910.1 Predicted CDS, f-box domain co...	21	2733
gi 23613363 ref NP_703207.1 erythrocyte membrane protein 1...	21	2733
gi 22024157 ref NP_611024.2 CG12956-PA [Drosophila melanog...]	21	2733
gi 22988530 ref ZP_00033594.1 hypothetical protein [burkho...]	21	2733
gi 6537223 gb AAU13567.1 AF179376.2 Orie2 [Mycoptasma ferme...]	21	2733
gi 28317234 gb AAU039624.1 GH04473p [Drosophila melanogaster]	21	2733
gi 31072003 cpe DAA01353.1 TPA: DEFP106-like protein [Papi...]	21	2733
gi 9629715 ref NP_045007.1 putative viral coat protein dup...	21	2733
gi 9629715 ref NP_045007.1 putative viral coat protein dup...	21	2733
gi 2385025 gb AAU61653.1 AF206304.4 ORP52 [Human herpesviru...]	21	2733
gi 31196503 ref XP_307099.1 ENSAAGP0000022845 [Anopheles ...]	21	2733
gi 21687143 ref NP_612204.1 RNase 8, placental [Homo sapie...]	21	2733
gi 15088547 gb AAU4083.1 AF136781.9 transcriptional activator	21	2733
gi 666132 gb AAU2240.1 transcriptional activator	21	2733
gi 10176803 dbj BAB09991.1 mutator-like transposase-like [...]	19	8859
gi 32404470 ref XP_322848.1 predicted protein [Neurospora ...]	19	8859
gi 21362028 ref NP_078933.2 hypothetical protein PJ11565 ...	19	8859

gi 18253397 gb AA166410.1	NPY receptor [Lampetra fluviatilis]	19	8859
gi 1755566 ref NP_497427.1	Putative nuclear protein, with...	19	8859
gi 21492735 ref NP_659810.1	unknown [Rhizobium etli] >gi 1...	19	8859
gi 20804175 emb CAD1378.1	PROBABLY NTP-SPECIFIC REGULATOR...	19	8859
gi 20892831 ref XP_153922.1	hypothetical protein XP_153922...	19	8859
gi 18643741 emb CAD23056.1	Colipase >gi 85421 pid 1A0533...	19	8859
gi 15668931 ref NP_247735.1	ferredoxin-type protein (napf)...	19	8859
gi 2858164 ref NP_135851.2	RITEN cDNA B93001H20 gene [Mu...	18	11887
gi 1962894 ref NP_004142.1	ribonucleotide reductase, large...	18	11887
gi 13242411 ref NP_077434.1	ribonucleotide reductase, large...	18	11887
gi 30447766 ref XP_301761.1	similar to peptidyl-Pro cts tr...	18	11887
gi 24650121 ref NP_651480.1	CG14238-PA [Drosophila melanog...	18	11887
gi 15238307 ref NP_199032.1	family tr l1pase EXL3, putativ...	18	11887
gi 20090513 ref NP_615588.1	hypothetical protein (multi-do...	18	15950
gi 29733668 ref XP_291251.1	similar to ADAM 7 precursor (A...	18	15950
gi 485335 gb AA25025.1	ureg	18	15950
gi 27703880 ref XP_230727.1	similar to defensin, beta 129;...	18	15950
gi 31239543 ref XP_320185.1	ENSANGP0000011153 [Anopheles ...	18	15950
gi 26352394 db BAC39827.1	unnamed protein product [Mus mu...	18	15950
gi 32480006 emb CA01650.1	OSJNB002110.14 [Oriza sativa ...	18	15950
gi 63219931 ref NP_012067.1	Involved in Processing ITS2; Yh...	18	15950
gi 13999319 sp O61129 CFM1_MOUSE	Complement factor 1 precu...	18	15950
gi 17461179 ref XP_066597.1	similar to tyrosine 3/tyrptoph...	18	15950
gi 15611134 ref NP_222785.1	UREASE ACCESSORY PROTEIN [Heli...	18	15950
gi 31230405 ref XP_321957.1	ENSANGP0000013922 [Anopheles ...	18	15950
gi 13147734 gb AA99804.1	220 kDa silk protein	18	15950
gi 1730843 sp P40798 SRC_DROME	Shuttle crat protein >gi 751...	18	15950
gi 31207579 ref XP_312756.1	ENSANGP000001442 [Anopheles ...	18	15950
gi 20137229 sp O28475 AD07_MACFA	ADAM 7 precursor (A distict...	18	15950
gi 16758958 ref NP_446081.1	foliistatin-like 3 [Rattus nor...	18	15950
gi 15031701 ref NP_005851.1	foliistatin-like 3 glycoprotei...	18	15950
gi 20901710 ref XP_156971.1	hypothetical protein XP_156971...	18	15950
gi 6324605 ref NP_014674.1	Metallothionein-like protein; C...	18	15950
gi 23021838 ref XP_00061491.1	hypothetical protein [Clostr...	18	15950
gi 13878203 ref NP_113557.1	foliistatin-like 3; E030038673...	18	15950
gi 27731549 ref XP_218624.1	similar to adaptor-related pro...	18	15950
gi 3643253 gb AAC36742.1	sperm maturation-related glycopro...	18	15950
gi 20137479 sp O28475 AD07_HUMAN	ADAM 7 precursor (A distict...	18	15950
gi 15899907 ref NP_344512.1	Conserved hypothetical protein...	18	15950
gi 13162353 ref NP_077071.1	complement factor 1 [Rattus no...	18	15950
gi 28511186 ref XP_289852.1	similar to H-2 class I histoco...	18	15950
gi 2739186 gb AA994621.1	glycoprotein A [Pneumocystis cari...	18	15950
gi 15644698 ref NP_206868.1	urase accessory protein (ureg...	18	15950
gi 3238876 emb CAD9836.1	similar to glycogen debranching...	18	15950
gi 24651113 ref NP_651716.1	CG1964-PA [Drosophila melanoga...	18	15950
gi 27718485 ref XP_235189.1	similar to 60S RIBOSOMAL PROTE...	18	15950
gi 16671561 ref NP_031484.1	adaptor protein complex AP-2, a...	18	15950
gi 11523717 ref NP_197688.1	expressed protein [Arabidopsis...	18	15950
gi 13309738 emb CAD4484.1	laccase [Gaumannomyces gramin...	18	15950
gi 28475506 gb AAH43207.1	Unknown (protein for IMAGE:52950...	18	15950
gi 27497797 gb AAH3155.1	substrate adhesion molecule prec...	18	15950

gi 5913966 db BAA84537.1	urease G [Helicobacter pylori]	18	15950
gi 4926957 gb AAH32965.1	complement factor 1 [Mus musculus]	18	15950
gi 416704 sp O23376 BAR3_CHITRE	Balbiant RING protein 3 prec...	18	15950
gi 22946527 gb AAH10891.1	CG3647-PA [Drosophila melanogaster]	18	15950
gi 11359837 db T744598	hypothetical protein (imported) - f...	18	15950
gi 31202839 ref XP_310268.1	ENSANGP0000015231 [Anopheles ...	18	15950
gi 24213057 ref NP_710538.1	conserved hypothetical protein...	18	15950
gi 31195615 ref XP_306755.1	ENSANGP0000013672 [Anopheles ...	18	15950
gi 13266641 db BAA26002.1	similar to adenyl cyclase asso...	18	15950
gi 22164216 gb AAH3613.1	AF483691.1 putative secreted prot...	18	15950
gi 22164198 gb AAH3604.1	AF483682.1 laccase (Gaumannomyces gramin...	18	15950
gi 19171194 emb CAD10747.1	laccase (Gaumannomyces gramin...	18	15950
gi 66717244 ref NP_031712.1	complement component factor 1 [...	18	15950
gi 19343434 ref NP_597914.1	polymetase [Northern cereal mo...	18	15950

Alignments

Get selected sequences Selected all Deselect all

>gi|17991441|gb|AAH51006.1|AF454393.1 foliistatin [Drosophila melanogaster]
Length = 705

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
Sbjct: 542 CKNSC 546

>gi|23822094|sp|O28528|RN58_PANTR Ribonuclease 8 precursor (RNase 8)
gi|19525682|gb|AAH96445.1|AF473855.1 RNase 8 [Pan troglodytes]
Length = 157

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
Sbjct: 92 CKNSC 96

>gi|17508299|ref|NP_490910.1 Predicted CDS, f-box domain containing protein 1
[Caenorhabditis elegans]
gi|17505688|db|AAH96445.1|AF473855.1 hypothetical protein M01D7.1 - Caenorhabditis elegans
gi|2105486|gb|AAH96068.1 hypothetical protein M01D7.1 [Caenorhabditis elegans]
Length = 339

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)
Query: 3 CKNSC 7

CKNSC
Sbjct: 46 CKNSC 50

>gi|23613363|ref|NP_703207.1| erythrocyte membrane protein 1 (PFEMP1) [Plasmodium falciparum]
gi|7670005|emb|CA889209.1| erythrocyte membrane protein 1 (PFEMP1) [Plasmodium falciparum]
Length = 2163

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
Sbjct: 633 CKNSC 637

>gi|22024157|ref|NP_611024.2| CG12956-PA [Drosophila melanogaster]
gi|21627146|gb|AAFS8157.2| CG12956-PA [Drosophila melanogaster]
Length = 581

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
Sbjct: 475 CKNSC 479

>gi|22988530|ref|ZP_00033594.1| hypothetical protein [Burkholderia fungorum]
Length = 416

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
Sbjct: 58 CKNSC 62

>gi|5537223|gb|AAFI5567.1|AF179376.2 ORF2 [Mycoplasma fermentans]
Length = 48

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
Sbjct: 28 CKNSC 32

>gi|28317234|gb|AAO39624.1| GH04473p [Drosophila melanogaster]
Length = 767

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
Sbjct: 604 CKNSC 608

>gi|31072003|tpg|DAA01353.1| TPA: DEFBI06-1-like protein [Papio anubis]
Length = 57

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
Sbjct: 33 CKNSC 37

>gi|9629715|ref|NP_045007.1| putative viral coat protein duplicate (CPd) [Littorina saxatilis]
gi|1620423|emb|CA63729.1| ORF4, putative viral coat protein duplicate gene [Littorina saxatilis]
gi|2398674|emb|CAA71290.1| putative viral coat protein duplicate (CPd) [Littorina saxatilis]
Length = 664

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
Sbjct: 286 CKNSC 290

>gi|9629715|ref|NP_045007.1| DNA helicase-primase complex [Human herpesvirus 3]
gi|136804|gb|F09300|HERA_VZVD DNA HELICASE/PRIMASE COMPLEX ASSOCIATED PROTEIN
gi|173884|gb|W2852 gene 52 protein - human herpesvirus 3
gi|60041|emb|CAA27935.1| ORF 52 (A1-771) [Human herpesvirus 3]
Length = 771

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
Sbjct: 43 CKNSC 47

>gi|7385025|gb|AAE61653.1|AE206304_4 ORF52 [Human herpesvirus 3]
Length = 771

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
Sbjct: 3 CKNSC 7

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Sbjct: 43 CRNSC 47

[>gi|31196303|ref|XP_307099.1| ENSANGP0000022845 [Anopheles gambiae]
gi|30179369|gb|EAA45752.1| ENSANGP0000022845 [Anopheles gambiae str. FEST]
Length = 182

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CRNSC 7

Sbjct: 141 CRNSC 145

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CRNSC 7

Sbjct: 81 CRNSC 85

[>gi|21687143|ref|NP_612204.1| **1** RNase 8, placental [Homo sapiens]
gi|23822095|dp|O87DE3|RNase_HUMAN **2** Ribonuclease 8 precursor (RNase 8)
gi|13525680|gb|AA189644.1|AF473854.1 **3** RNase 8 [Homo sapiens]
Length = 154

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CRNSC 7

Sbjct: 89 CRNSC 93

[>gi|15088547|gb|AAK84083.1|AF326781.2 putative resistance protein [Triticum mon
Length = 907

Score = 20.6 bits (41), Expect = 2733
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 3 CRNSC 7

Sbjct: 278 CRNSC 282

[>gi|666132|gb|AA62240.1| transcriptional activator
Length = 584

Score = 18.9 bits (37), Expect = 8859
Identities = 5/6 (83%), Positives = 5/6 (83%)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

Query: 1 FCCKNS 6

Sbjct: 469 FCCKNS 474

[>gi|10176803|dbj|BAB09991.1| mutator-like transposase-like [Arabidopsis thaliana]
Length = 825

Score = 18.9 bits (37), Expect = 8859
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 1 FCCKNS 7

Sbjct: 548 FCCKNS 554

[>gi|32404470|ref|XP_322848.1| predicted protein [Neurospora crassa]
gi|28918646|gb|BA129063.1| predicted protein [Neurospora crassa]
Length = 705

Score = 18.9 bits (37), Expect = 8859
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 1 FCCKNS 7

Sbjct: 386 FCCKNS 392

[>gi|21362028|ref|NP_078933.2| **1** hypothetical protein FLJ11565 [Homo sapiens]
gi|15551580|dbj|BAB71125.1| **2** unnamed protein product [Homo sapiens]
Length = 760

Score = 18.9 bits (37), Expect = 8859
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FCCKNS 6

Sbjct: 145 FCCKNS 150

[>gi|18253297|gb|AA166410.1| NPY receptor [Lampetra fluviatilis]
Length = 365

Score = 18.9 bits (37), Expect = 8859
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FCCKNS 6

Sbjct: 358 FCCKNS 363

[>gi|17555666|ref|NP_497427.1| **1** Putative nuclear protein, with a coiled coil-4 c
specific [Caenorhabditis elegans]

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

gi|131545438|db|AAK84598.1|AC084353.16 Hypothetical protein Y2277A.9 [Caenorhabditis]

Length = 668

Score = 18.9 bits (37), Expect = 8859
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FCCKNS 6

F CKNS

Sbjct: 435 FCCKNS 440

Score = 18.9 bits (37), Expect = 8859
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FCCKNS 6

F CKNS

Sbjct: 323 FCCKNS 328

gi|21492735|ref|NP_659810.1| unknown [Rhizobium etli]
gi|17092731|sp|P54931|NTPA_RHIF Nit-specific regulatory protein
gi|1144325|gb|AA84917.1| NitA
gi|21467160|gb|AA854823.1| unknown [Rhizobium etli]
Length = 584

Score = 18.9 bits (37), Expect = 8859
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FCCKNS 6

F CKNS

Sbjct: 469 FCCKNS 474

gi|20804175|emb|CAD31378.1| PROBABLE NIT-SPECIFIC REGULATORY PROTEIN ACTIVATOR
DNA-BINDING NITFA [Mesorhizobium loti]
Length = 586

Score = 18.9 bits (37), Expect = 8859
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FCCKNS 6

F CKNS

Sbjct: 469 FCCKNS 474

gi|20892831|ref|XP_153922.1| hypothetical protein XP_153922 [Mus musculus]
Length = 115

Score = 18.9 bits (37), Expect = 8859
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FCCKNS 6

F CKNS

Sbjct: 104 FCCKNS 109

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

gi|116902|sp|P11149|COL_SQUAC Colipase
gi|85421|pir|A05331 colipase - spiny dogfish (fragment)
Length = 39

Score = 18.9 bits (37), Expect = 8859
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 1 FCCKNSC 7

F CK+SC

Sbjct: 20 FCCKNSC 26

gi|18643741|emb|CAD23056.1| dJ75H8.2 (similar to KIAA0136 protein) [Homo sapiens]
Length = 903

Score = 18.9 bits (37), Expect = 8859
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FCCKNS 6

F CKNS

Sbjct: 288 FCCKNS 293

gi|15668931|ref|NP_247735.1| ferredoxin-type protein (napH) [Methanococcus jan
gi|2128473|pir|F64393 hypothetical protein MJ0750 - Methanococcus jannaschii
gi|1592304|gb|AA898746.1| ferredoxin-type protein (napH) [Methanococcus jannaschii]
Length = 238

Score = 18.9 bits (37), Expect = 8859
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 1 FCCKNSC 7

F CK+SC

Sbjct: 217 FCCKNSC 223

gi|28528164|ref|XP_135851.2| RIKEN CDNA B930011H20 gene [Mus musculus]
gi|31542182|ref|NP_848897.2| RIKEN CDNA B930011H20 gene [Mus musculus]
gi|26348945|dbj|BAC38112.1| unnamed protein product [Mus musculus]
Length = 1358

Score = 18.5 bits (36), Expect = 11887
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FCCKNS 6

F CKNS

Sbjct: 671 FCCKNS 676

gi|19625894|ref|NP_040142.1| ribonucleotide reductase, large subunit (human he
gi|132612|sp|P09248|RIH1_VZVD RIBONUCLEOTIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (R
REDUCTASE)

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

7/10/2003

gi|66405|pir||WHEB19 ribonucleoside-diphosphate reductase (BC 1.17.4.1) large cha
human herpesvirus 3
gi|60008|emb|CA27902.1| ORF19 (AA1-775) [Human herpesvirus 3]
Length = 775

Score = 18.5 bits (36), Expect = 11887
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 1 FXCKNSC 7
F CK SC
Sbjct: 487 FCKKSC 493

gi|13242411|ref|NP_077434.1| ribonucleotide reductase, large subunit [Cercopit
71
gi|11036563|gb|AA627192.1|AF275348_12 ribonucleotide reductase, large subunit [Ce
71
Length = 783

Score = 18.5 bits (36), Expect = 11887
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 1 FXCKNSC 7
F CK SC
Sbjct: 495 FCKKSC 501

gi|3014756|ref|XP_301761.1| similar to peptidyl-Pro cis trans isomerase [H
Length = 208

Score = 18.5 bits (36), Expect = 11887
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 1 FXCKNSC 7
F CK SC
Sbjct: 119 FACKGSC 125

gi|24650321|ref|NP_651480.1| CG14238-PA [Drosophila melanogaster]
gi|7301471|gb|AA956595.1| CG14238-PA [Drosophila melanogaster]
Length = 523

Score = 18.5 bits (36), Expect = 11887
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6
F CKNS
Sbjct: 296 FCKKNS 301

gi|15238307|ref|NP_199032.1| family II lipase EXL3, putative [Arabidopsis thal;
gi|9757962|dbj|BA08450.1| GDSL-motif lipase/hydrolase-like protein [Arabidopsis
Length = 319

Score = 18.5 bits (36), Expect = 11887
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6
F CKNS
Sbjct: 282 FCKKNS 287

gi|20090513|ref|NP_616588.1| hypothetical protein (multi-domain) [Methanosarci
str. C2A]
gi|19915538|gb|AA05068.1| hypothetical protein (multi-domain) [Methanosarcina ac
str. C2A]
Length = 955

Score = 18.0 bits (35), Expect = 15950
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6
F CKNS
Sbjct: 361 FCKKNS 366

gi|29733668|ref|XP_291251.1| similar to ADAM 7 precursor (A disintegrin and r
domain 7) (Sperm maturation-related glycoprotein GP-83)
[Homo sapiens]
Length = 754

Score = 18.0 bits (35), Expect = 15950
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6
F CKNS
Sbjct: 490 FCKKNS 495

gi|485335|gb|AA25025.1| ureg
Length = 199

Score = 18.0 bits (35), Expect = 15950
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6
F CKNS
Sbjct: 46 FCKKNS 51

gi|27703880|ref|XP_230727.1| similar to defensin, beta 129, defensin, beta 2;
open reading frame 87 [Homo sapiens] [Rattus
norvegicus]
Length = 164

Score = 18.0 bits (35), Expect = 15950
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7

CR+SC
Sbjct: 34 CRDSC 38

>gi|31239543|ref|XP_320185.1| ENSANGP00000011153 [Anopheles gambiae]
gi|30174007|gb|EAA00393.2| ENSANGP00000011153 [Anopheles gambiae str. PEST]
Length = 4569

Score = 18.0 bits (35), Expect = 15950
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6
F CKNS
Sbjct: 1014 FXCKNS 1019

>gi|2635394|db|BAC39827.1| unnamed protein product [Mus musculus]
Length = 257

Score = 18.0 bits (35), Expect = 15950
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
CK+SC
Sbjct: 93 CKDSC 97

>gi|3248006|emb|CA01650.1| OSJNB0021110.14 [Oryza sativa (japonica cultivar-group
gi|32480127|emb|CA01940.1| OSJNB0073113.2 [Oryza sativa (japonica cultivar-group
Length = 459

Score = 18.0 bits (35), Expect = 15950
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
CK+SC
Sbjct: 306 CRDSC 310

>gi|6321921|ref|NP_012067.1| Involved in processing INS2; Yhr197wp [Saccharomyces
gi|7317661|sp|P38883|YH27_YEAST HYPOTHETICAL 86.7 KD PROTEIN IN EGD-2/SUN1 INTERGEN
gi|6266991|pir||S46678 hypothetical protein YHR197w - yeast (Saccharomyces cerevisiae
gi|458930|gb|AA06356.1| Yhr197wp [Saccharomyces cerevisiae]
Length = 763

Score = 18.0 bits (35), Expect = 15950
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6
F CKNS
Sbjct: 514 FXCKNS 519

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi

7/10/2003

>gi|13959319|sp|Q61129|CPAI_MOUSE Complement factor I precursor (C3B/C4B inacti
Length = 603

Score = 18.0 bits (35), Expect = 15950
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6
F CKNS
Sbjct: 142 FXCKNS 147

>gi|17461179|ref|XP_066597.1| similar to tyrosine 3/tryptophan 5 -monooxygenat
protein-1; phospholipase A2; 14-3-3 zeta (Homo sapiens)
Length = 118

Score = 18.0 bits (35), Expect = 15950
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
CK+SC
Sbjct: 113 CRDSC 117

>gi|15611134|ref|NP_222785.1| UREASE ACCESSORY PROTEIN [Helicobacter pylori 399;
gi|7388360|sp|Q92M27|UREG_HBRLPU Urease accessory protein ureg
gi|17447446|pir||C71979 urease accessory protein ureg [similarity] - Helicobacter
(strain 399)
gi|4154571|gb|AA05647.1| UREASE ACCESSORY PROTEIN [Helicobacter pylori 399]
Length = 199

Score = 18.0 bits (35), Expect = 15950
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FXCKNS 6
F CKNS
Sbjct: 46 FXCKNS 51

>gi|31243045|ref|XP_321957.1| ENSANGP00000013922 [Anopheles gambiae]
gi|21289514|gb|EAA01807.1| ENSANGP00000013922 [Anopheles gambiae str. PEST]
Length = 1557

Score = 18.0 bits (35), Expect = 15950
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CKNSC 7
CK+SC
Sbjct: 1529 CRDSC 1533

>gi|1314734|gb|AA09804.1| 220 kDa silk protein
Length = 1704

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi

7/10/2003

Score = 18.0 bits (35), Expect = 15950
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CRNSC 7
 CR+SC
 Sbjct: 312 CRDSC 316

gi|210843|sp|P40798|SNC_DROME Shuttle craft protein - fruit fly (Drosophila melanogaster)
 gi|7511869|pir|I13338 gene shuttle craft protein [Drosophila melanogaster]
 gi|487400|db|AB060255.1 shuttle craft protein [Drosophila melanogaster]
 Length = 1106

Score = 18.0 bits (35), Expect = 15950
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CRNSC 7
 CR+SC
 Sbjct: 590 CRDSC 594

Score = 18.0 bits (35), Expect = 15950
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CRNSC 7
 CR+SC
 Sbjct: 575 CRDSC 579

gi|31207579|ref|XP_312756.1| ENSANGP00000003142 [Anopheles gambiae]
 gi|30177153|gb|EAA08447.2| ENSANGP00000003142 [Anopheles gambiae str. PEST]
 Length = 1204

Score = 18.0 bits (35), Expect = 15950
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CRNSC 7
 CR+SC
 Sbjct: 678 CRDSC 682

gi|20137329|gb|Q28475|AD07_MACFA ADAM 7 precursor (A disintegrin and metalloprotease)
 (epididymal apical protein 1) (EAP 1)
 gi|283937|pir|I528258 androgen-regulated epididymal protein precursor - crab-eati
 macaque
 gi|38063|emb|CAA4929.1 epididymal apical protein I-precursor [Macaca fascicularis]
 Length = 776

Score = 18.0 bits (35), Expect = 15950
 Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 1 FCKNS 6
 F CKNS
 Sbjct: 490 FCKNS 495

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

gi|16758958|ref|NP_446081.1| Follistatin-like 3 [Rattus norvegicus]
 gi|23821549|sp|Q99PW7|PSL3_RAT Follistatin-related protein 3 precursor (Follistatin-related gene protein)
 gi|12964594|dbj|BAB32664.1| Follistatin-related protein FUKG [Rattus norvegicus]
 gi|23095929|dbj|BAC16229.1| Follistatin-like protein [Rattus norvegicus]
 Length = 236

Score = 18.0 bits (35), Expect = 15950
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 CRNSC 7
 CR+SC
 Sbjct: 93 CRDSC 97

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PIR
 Posted date: Jul 10, 2003 1:49 AM
 Number of letters in database: 474,244,320
 Number of sequences in database: 1,477,204

Lambda	K	H
0.366	0.280	2.29
Gapped	K	H
0.294	0.110	0.610

Matrix: PAM30
 Gap Penalties: Existence: 9, Extension: 1
 Number of Hits to DB: 3,751,296
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 Number of sequences better than 20000.0: 85
 Number of HSP's better than 20000.0 without gapping: 85
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
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 Length of query: 7
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 effective search space: 4268198880
 effective search space used: 4268198880
 T: 11
 A: 40
 X1: 14 (7.4 bits)
 X2: 35 (14.8 bits)

<http://www.ncbi.nlm.nih.gov/Blast.cgi>

7/10/2003

X3: 58 (24.6 bits)
S1: 35 (20.3 bits)
S2: 35 (18.0 bits)

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igin for the loris-lemur clade cannot be ruled out (24) in the light of this new discovery. A similar scenario (adapted from molecular data) has been suggested for endemic Malagasy rodents (32).

The possibility that lemuriforms and lorisiforms originated in Asia rather than in Africa cannot be rejected without further paleontological evidence from both continents and from Madagascar. It must, however, be emphasized that their origin is undoubtedly as ancient as that of adapiforms (Fig. 3A). The discovery of a cheirogaleid-like lemur in Oligocene deposits of Pakistan suggests that whatever the timing and direction of faunal dispersions, South Asia was, as for anthropoids (33), an important theater of early strepsirrhine evolution, reflecting the complex role played by the drifting Greater India in the evolutionary history of Malagasy lemurs.

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36. We are indebted to Nawab Mohammad Akbar Khan Bugti, Lord of the Bugti Tribes, and to Shahid Hassan Bugti for their total fieldwork assistance, to I. Akhund for his help, and to Bahadur Khan Rodani, Vice Chancellor of the University of Balochistan. We thank R. D. Martin for providing us useful comments on the manuscript. Many thanks to C. Denys and J. Cuisin (MNHN, Paris) for access to comparative material and to B. Marandat for preparing fossils. This work was funded by the University of Montpellier (CNRS-UMR 5554), the MNHN, Paris (CNRS-UMR 8569), the Fyssen, Leakey, Wenner-Gren, Singer-Polignac, Bleustein-Blanchet and Treilles Foundations. This is ISEM publication 2001-107.

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Caenorhabditis elegans p53: Role in Apoptosis, Meiosis, and Stress Resistance

W. Brent Derry,* Aaron P. Putzke, Joel H. Rothman

We have identified a homolog of the mammalian p53 tumor suppressor protein in the nematode *Caenorhabditis elegans* that is expressed ubiquitously in embryos. The gene encoding this protein, *cep-1*, promotes DNA damage-induced apoptosis and is required for normal meiotic chromosome segregation in the germ line. Moreover, although somatic apoptosis is unaffected, *cep-1* mutants show hypersensitivity to hypoxia-induced lethality and decreased longevity in response to starvation-induced stress. Overexpression of CEP-1 promotes widespread caspase-independent cell death, demonstrating the critical importance of regulating p53 function at appropriate levels. These findings show that *C. elegans* p53 mediates multiple stress responses in the soma, and mediates apoptosis and meiotic chromosome segregation in the germ line.

The p53 tumor suppressor is among the most frequently mutated genes in human cancer and plays a critical role in maintaining genomic stability by regulating cell cycle progression and apoptosis in response to DNA damage (1, 2). Analysis of the mechanisms through which p53 integrates the cellular response to stress and damage in vivo has been limited by the absence of a genetic system. Recently, a p53 homolog was shown to participate in apoptosis induced by genotoxic stress in *Drosophila* (3–5) on the basis of forced expression of dominant negative forms; however, the organism-wide role of the gene could not be assessed in these experiments.

Standard searches of the genomic sequence suggested that *C. elegans* does not have a p53-like gene (6). However, using additional algorithms, we identified a *C. elegans* gene encoding a protein with signature sequences common to the p53 family, includ-

ing the residues most frequently mutated in human cancers (7). The cDNA sequence of this gene, *cep-1* (denoting *C. elegans* p53-like-1), predicts a 429-amino acid protein that is similar to the human protein in the NH₂-terminal transactivation domain and the highly conserved DNA binding domains (Fig. 1). CEP-1 appears to be the only p53 family member encoded in the *C. elegans* genome, which suggests that p53 paralogs (including p63 and p73) may have evolved from a single ancestor related to CEP-1.

To assess the in vivo function of *cep-1*, we isolated a chromosomal rearrangement, *cep-1(w40)* (8). This mutant strain contains an intact copy of *cep-1* at its normal genomic location; the *cep-1(w40)* mutant gene, which encodes a truncated protein lacking the DNA binding domain, is translocated elsewhere in the genome. Although they exhibit impenetrant (~2%) embryonic lethality, *cep-1(w40)* mutants are generally viable and fertile. Moreover, depleting *cep-1* function by RNA interference (RNAi) (9) similarly leads to impenetrant embryonic lethality (Table 1). It is likely that RNAi results in a strong loss-of-function phenotype, as it eliminates detectable expression of a CEP-1::GFP

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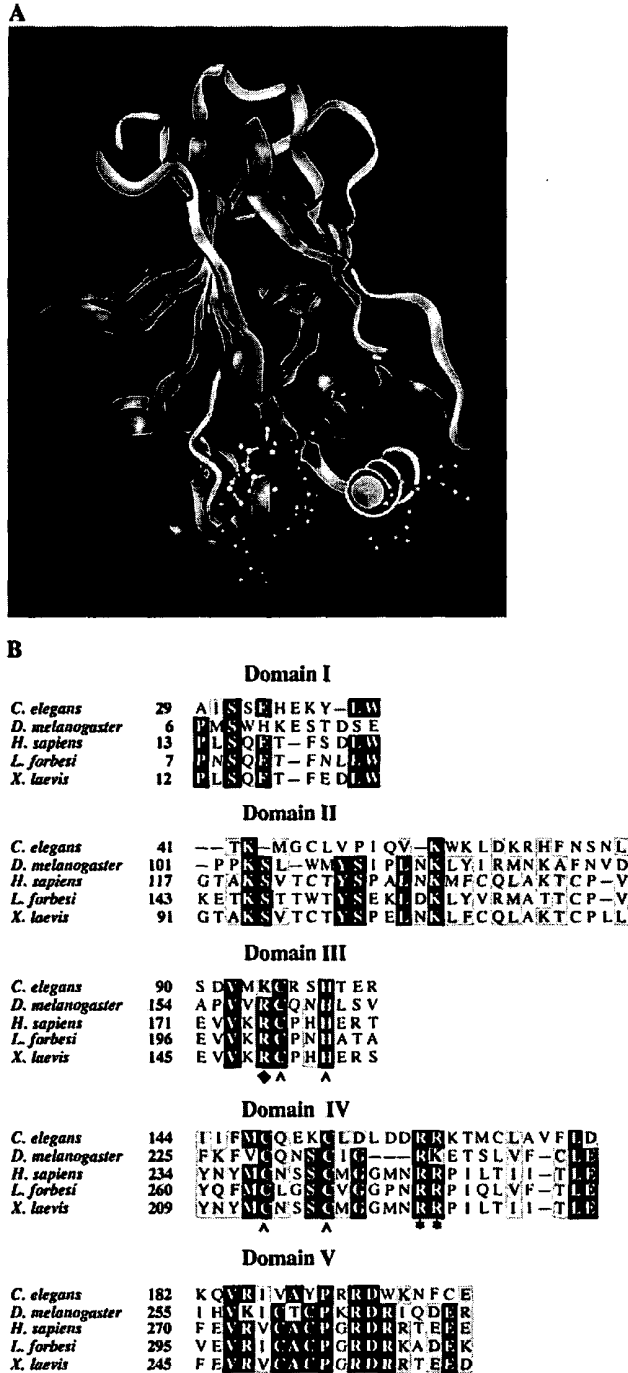
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(green fluorescent protein) reporter (10). We found that both *cep-1(w40)* and *cep-1(RNAi)* embryos undergo a normal pattern of somatic apoptosis, suggesting that CEP-1 is not re-

quired for developmental programmed cell death in the soma (10).

Unlike somatic cells, which have a fixed cell division program, germ-line nuclei in *C.*

elegans undergo indeterminate rounds of division and are subject to checkpoint control and apoptosis in response to genotoxic stresses (11); they also undergo developmentally programmed "physiological" cell death, which appears to be regulated by distinct



of Mdm-2 with human p53 (35, 36). The region of highest conservation lies in the DNA binding domain (domains II to V), where several amino acids have been shown to contact the major and minor grooves of the p53 binding site in the DNA-p53 cocrystal (34). These include four of the five most frequently mutated Arg residues in human cancer (asterisks), as well as Cys and His residues (carets) that make critical contacts with DNA in the three-dimensional structure of human p53. The fifth cancer "hot spot" Arg is conservatively substituted with a Lys in CEP-1 (diamond). The CEP-1 sequence corresponds to F5285.5 reported by the *C. elegans* Sequencing Consortium (GenBank accession number CAA99857).

Fig. 1. Conservation of transactivation and DNA binding domains in *C. elegans* CEP-1. (A) Low-resolution three-dimensional model of CEP-1 DNA binding domain (residues 22 to 197) created with the program Modeler/Insight II 98.0 (33). The coordinates of residues 108 to 298 from the crystal structure of the human p53 DNA binding domain were used as the template (34). Conserved Arg residues that make contact with the consensus DNA binding site and that are the most frequently mutated residues in human cancer are shown in red. Amino acids in yellow represent conserved Cys and His residues that coordinate a Zn ion. Portions of the structure shown in magenta are the β strands of the core domain. The green rod indicates the H2 helix that makes contacts with the DNA. (B) Alignment of conserved domains in p53 family members. Single-letter abbreviations for amino acid residues are as follows: A, Ala; C, Cys; D, Asp; E, Glu; F, Phe; G, Gly; H, His; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr. Black boxes indicate amino acids that are identical in at least four of the sequences; gray boxes indicate conservative substitutions. Several residues in the NH₂-terminal transactivation domain (domain I) are conserved in CEP-1, including Leu³⁹ and Trp³⁹, which are necessary for transcriptional activation and for the physical interaction

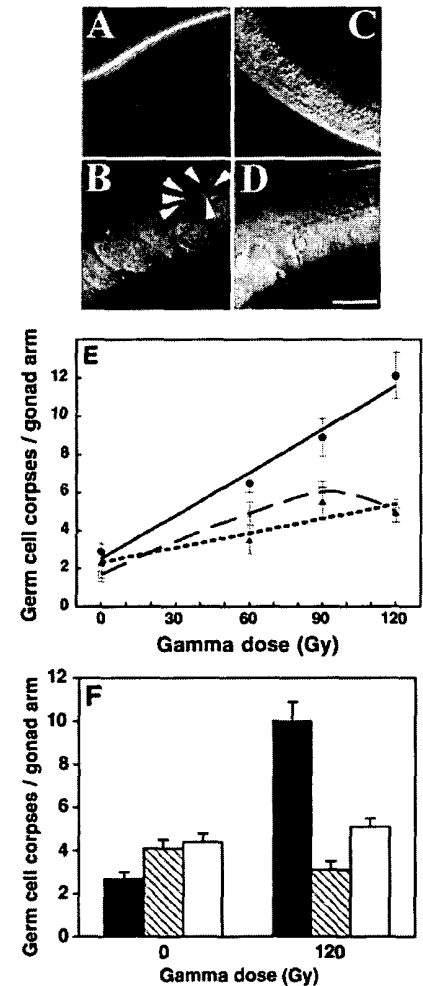


Fig. 2. Requirement of *cep-1* for normal activation of germ cell apoptosis in response to DNA damage. Shown are wild-type (A and B) and *cep-1(w40)* adults (C and D) observed by differential interference contrast (DIC) microscopy 12 hours after the L4 stage, either without radiation [(A) and (C)] or after exposure to 60-Gy IR [(B) and (D)]. Arrowheads point to germ cell corpses in a single focal plane. (E) Quantification of germ cell corpses with increasing doses of IR in wild-type (●), *cep-1(w40)* (▲), and *cep-1(RNAi)* adults (□). (F) Dominance of *cep-1(w40)* allele in suppressing DNA damage-induced germ cell apoptosis. Data are shown for wild type (solid bars), *cep-1(w40)* heterozygotes (hatched bars), and *cep-1(w40)* homozygotes (open bars) in the absence versus presence of 120-Gy IR. L4-stage hermaphrodites were irradiated with gamma rays from a ¹³⁷Cs source, and after 24 hours the number of apoptotic germ cells per gonad arm was determined in 10 to 15 animals. Error bars are SEM.

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signaling pathways upstream of the core apoptotic machinery (12). DNA damage activates germ cell apoptosis through a conserved checkpoint pathway that includes the *rad-5* and *mrt-2* genes and the gene altered by the *op241* mutation; however, none of these genes is required for physiological germ cell death (11). Because p53 coordinates cellular responses to DNA damage, we hypothesized that *cep-1* might regulate apoptosis in the germ line in response to genotoxic stress. Indeed, *cep-1(w40)* hermaphrodites are resistant to ionizing radiation (IR)-induced apoptosis of germ cells (Fig. 2), and *cep-1(RNAi)* phenocopies this effect of *w40* (Fig. 2E). This block in activation of the germ-line cell death program may be general to DNA damage because *cep-1(w40)* mutants, like *rad-5*, *mrt-2*, and *op241* mutants (11), also fail to undergo germ cell death induced by the DNA modifying compound *N*-ethyl-*N*-nitrosourea (10).

Our observations suggest that the truncated CEP-1(w40) protein interferes with the

proapoptotic activity of wild-type CEP-1. Both a heterozygous *w40* mutation and overexpression of the *cep-1(w40)* gene from a heat shock promoter in a wild-type background confer resistance to IR-induced germ cell apoptosis, confirming that *w40* dominantly attenuates wild-type *cep-1* function (Fig. 2F) (10).

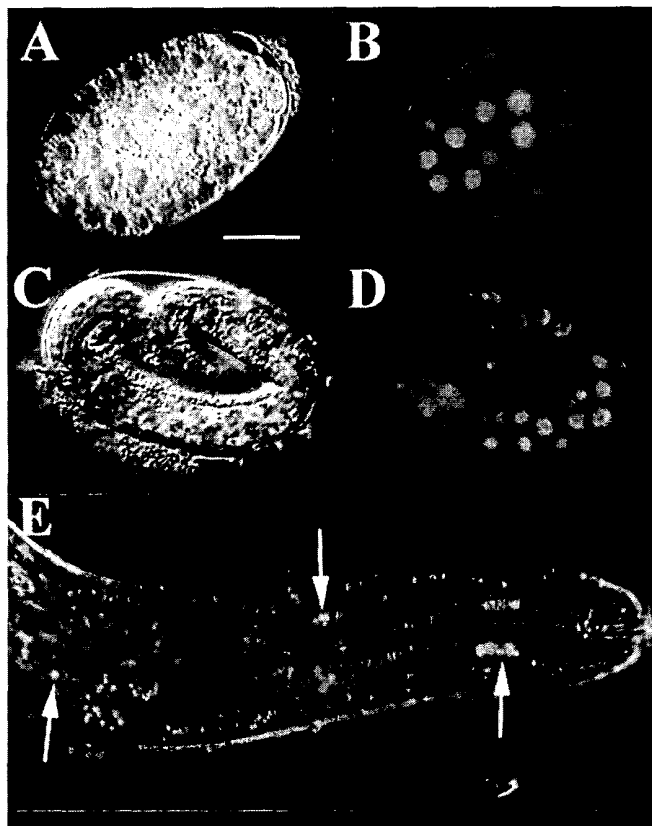
Unlike *rad-5*, *mrt-2*, and *op241* mutants, which are defective in both germ cell apoptosis and cell cycle checkpoint arrest induced by DNA damage, *cep-1(w40)* and *cep-1(RNAi)* germ cells undergo a transient cell cycle arrest in response to IR that is indistinguishable from that of the wild type (10). Furthermore, ectopic expression of CEP-1 in early embryos fails to cause cell division arrest. This ability to activate apoptosis but not arrest the cell cycle is a property shared by *Drosophila* p53, but not vertebrate homologs (3, 4), possibly revealing a primordial role for p53 proteins in apoptosis specifically.

Analysis of animals depleted for *cep-1*

function also uncovered a meiotic role in the absence of genotoxic stress. Nondisjunction of the X chromosome at meiosis I in the hermaphrodite germ line generates nullo-X gametes, leading to XO male progeny (13). We found that depletion of *cep-1* function by RNAi causes an increase in production of males (the Him phenotype, for high incidence of males) under normal growth conditions (Table 1). This effect was observed uniformly among broods of individual hermaphrodites, which implies that *cep-1* is required for chromosome segregation during meiosis rather than during the mitoses preceding meiosis. Mitotic proliferation of nuclei missing an X chromosome would be expected to produce much more variable broods, some with very high numbers of males. The *cep-1(w40)* mutant does not show a Him phenotype, which suggests that the truncated protein does not interfere with the meiotic chromosome segregation activity of CEP-1.

The low frequency of embryonic lethality in *cep-1* mutants (Table 1) might result from

Fig. 3. Expression and requirement of *cep-1* in somatic cells. (A to E) Zygotic expression pattern of a CEP-1::GFP fusion reporter in embryos and larvae. Shown are DIC (A and C) and fluorescence (B and D) images of embryos at ~50-cell (A and B) and pretzel (C and D) stages. Similar expression patterns were observed in six independent lines (10). Scale bar, ~10 μ m. (E) Overlay of GFP and DIC images of CEP-1 expression in pharynx after hatching. Anterior is to the right. Arrows point to nucleolar localization of CEP-1::GFP in anterior m2 muscle cells and other pharyngeal muscle and neurons of an L3-stage hermaphrodite. (F) Lethality of wild-type (solid bars) and *cep-1(w40)* embryos (hatched bars) under normoxic (21% O₂) and hypoxic (0.5% O₂) conditions. Early embryos were placed in chambers maintained with a constant atmosphere at the indicated oxygen concentration, as measured with a Systech oxygen analyzer. Lethality (percent \pm SEM) was scored by quantifying the number of surviving adults arising from a known number of embryos. (G) Effect of prolonged L1 starvation on survival to adulthood of *cep-1(w40)* (■) and wild-type larvae (□). Embryos were collected from gravid adults by hypochlorite treatment and hatched in M9 buffer with cholesterol (10 μ g/ml) at 20°C in the absence of food. Aliquots of arrested L1 larvae were taken every 72 hours and grown on NGM plates with OP50 bacteria. The fraction surviving to adulthood was determined after 3 days of growth at 20°C. We observed a slight increase in the number of



wild-type surviving adults between 6 and 9 days; this likely reflects sticking of some larvae to the culture tube at earlier time points. (H) Quantification of apoptotic death throughout embryonic stages after overexpression of CEP-1 (hatched bars) compared with overexpression of CEP-1(w40) (solid bars) by heat shock. Embryos between the 50- and 100-cell stage were collected from gravid adults and heat-shocked at 34°C for 15 min; cell corpses were quantified as the embryos developed. Error bars are SEM.

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autosomal meiotic nondisjunction or could reflect an essential function during normal embryogenesis. Consistent with the latter notion, we found that zygotic expression of a CEP-1::GFP fusion reporter is first detected at the ~50-cell stage and appears to be ubiquitous throughout embryonic development (14) (Fig. 3, A to D). Near the end of embryogenesis, GFP fluorescence decreases; after hatching, expression is restricted to a subset of pharynx cells, becoming concentrated in nucleoli (Fig. 3E).

Although little is known about the role of p53 in embryogenesis, knockout mice have revealed a role in normal development (15). p53 is also highly expressed embryonically in mice and frogs; however, its precise role during embryogenesis remains unclear (16–18). The high levels of ubiquitous CEP-1 expression in *C. elegans* might serve a protective function during embryogenesis, when cell division is rapid and replication errors are likely to occur at a higher frequency. However, *cep-1(w40)* embryos and larvae are not resistant to IR, the intensity and pattern of CEP-1::GFP expression does not change in response to this treatment, and the pattern of apoptosis in *cep-1(w40)* or *cep-1(RNAi)* embryos is indistinguishable from that of the wild type (10). Thus, the proapoptotic function of CEP-1 may be restricted to germ-line cells. Because somatic cells in *C. elegans* cannot generally be replaced if damaged, and arise by a determinate number of cell divisions (and hence are less likely to become tumorous), damage-induced apoptosis in the soma could be detrimental to the animal. In contrast, the germ line contains an excess of germ cells that are not used in self-fertilizing hermaphrodites, and damaged germ cells that are not eliminated could result in defective progeny, making it desirable to eliminate these expendable cells.

Because the DNA damage checkpoint function of CEP-1 is apparently restricted to the germ line, we reasoned that somatic CEP-1 might instead activate a response to other stresses. In vertebrates, p53 is activated by diverse stress signals, including hypoxia,

which leads to stabilization of the protein (19, 20). As a soil-dwelling nematode, *C. elegans* is likely to encounter hypoxic environments frequently. Indeed, we found that *cep-1(w40)* mutants are hypersensitive to the lethal effects of hypoxia (Fig. 3F).

Under conditions of starvation stress, *C. elegans* first-stage (L1) larvae undergo developmental arrest until food is available. We found that the life-span of *cep-1(w40)* larvae is reduced relative to the wild type when they were starved at the L1 stage (Fig. 3G). Wild-type survival was reduced by 50% after ~14 days, whereas survival of *cep-1(w40)* larvae was reduced by the same magnitude after only ~9 days (Fig. 3G). In contrast, we found that the life-span of mutant animals during normal growth was unaffected (10). The effect of starvation- and hypoxia-induced stress on *cep-1* mutants suggests that CEP-1 can modulate responses to both genotoxic stress in the germ line and environmental stress in the soma.

To address the importance of maintaining proper CEP-1 levels during development, we overexpressed CEP-1 from a heat shock-inducible promoter in 50- to 100-cell-stage embryos (21). The resultant embryos often arrested before hatching and showed severe morphological abnormalities. These embryos did not undergo cell cycle arrest, but they showed a significant increase in the number of cell corpses that accumulated throughout embryogenesis; some terminally arrested embryos contained as many as 40 cell corpses (Fig. 3H) at a time when wild-type animals contain virtually none. No apoptotic corpses were observed when CEP-1 was overexpressed in a mutant lacking CED-3 caspase function (10), which is required for all developmentally programmed cell deaths (22). CEP-1-overexpressing embryos that underwent apparently normal development, and that did not show significantly elevated numbers of cell corpses, nevertheless invariably succumbed, arresting before hatching or as L1 larvae with widespread signs of necrosis. Indeed, overexpression of CEP-1 at all larval stages and during adulthood also caused pen-

etrant lethality and widespread necrotic cell death, independent of CED-3 caspase function. All larvae overexpressing the protein became uncoordinated within 8 hours after induction of *cep-1* overexpression and eventually degenerated.

The lethality of overexpressed CEP-1 appears to be a specific effect, as it requires an intact DNA binding domain; overexpression of the truncated *cep-1(w40)* allele resulted in virtually no effect on viability. Moreover, we found that expression of human p53 results in similar degenerative phenotypes in *C. elegans* embryos and larvae (10), which suggests that human p53 and nematode CEP-1 can perform similar biochemical functions. The lethality of overexpressed *cep-1* does not appear to result from activation of the core apoptotic machinery, because mutations in *ced-3* or *ced-4* (22) did not block these effects (10). However, dying animals contained large numbers of nuclei that stained positive for acridine orange, generally regarded as a marker of apoptosis (23). Therefore, high levels of CEP-1 may override the requirement for the CED-3 caspase and activate a caspase-independent cell death program, perhaps analogous to the caspase-independent apoptosis observed recently in other systems, which is revealed when caspase function is blocked in cells otherwise programmed to die (24).

We find that *C. elegans* p53 functions both during normal development (e.g., to ensure proper meiotic chromosome segregation) and under conditions of cellular and genotoxic stress (e.g., in response to DNA damage, hypoxia, or starvation). Although it is expressed ubiquitously in embryos, *cep-1* must be carefully regulated because elevated levels of CEP-1 protein are invariably lethal. It should now be possible to use *C. elegans* as a genetic system to screen for modifiers of the *cep-1* mutant phenotype, allowing a comprehensive dissection of the pathways through which p53-like proteins function to mediate stress response, to activate germ-line apoptosis, and to regulate meiotic chromosome segregation.

Table 1. Elimination of *cep-1* function causes meiotic X chromosome nondisjunction.

Genotype	Total F ₁ 's	Total dead eggs	Percent dead eggs	Total males*	Percent males
<i>unc-22(RNAi)</i> †	3971	32	0.8	2	0.1
<i>cep-1(RNAi)</i> †	2355	113	4.8	33	1.4
N2‡	2464	2	0.08	4	0.2
<i>cep-1(w40)</i> ‡	3286	38	1.2	10	0.3

*Males produced by *cep-1(RNAi)* hermaphrodites mated normally and produced the expected frequency of male cross progeny (10), implying that CEP-1 is needed for a function in normal meiotic chromosome segregation and not for sexual identity per se. †Between 15 and 20 L4-stage N2 hermaphrodites were soaked in *cep-1* double-stranded RNA (~5 mg/ml) for 16 to 18 hours at 20°C. Soaked adults were transferred every 24 hours, and dead eggs, males, and hermaphrodites were scored in the F₁ generation. *unc-22(RNAi)* was used as a negative control; although this RNAi treatment invariably results in a penetrant *Unc-22* phenotype, no significant effect on male production or viability was seen. ‡N2 (wild-type) and *cep-1(w40)* strains were soaked in M9 buffer for 16 to 18 hours at 20°C and scored as described above.

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7. The amino acid sequence of squid (*Loligo forbesi*) p53 (U43595) was used as a query to search the *C. elegans* database with the PSI-BLAST algorithm (25). Several low-scoring *C. elegans* open reading frames were identified and aligned with several p53 family members using the Block Maker tool (26). F52B5.5 was the only predicted *C. elegans* gene identified with the appropriate p53 signature sequences in the correct modular order. There are seven exons in *cep-1*, and the intron-exon boundaries are in similar positions to those in the murine and human

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- p53 genes (27, 28), underscoring their evolutionary relatedness.
8. We screened 48,000 wild-type (N2) genomes for a *cep-1* deletion using 4,5',8-trimethylpsoralen/ultraviolet light mutagenesis as described (29, 30). First-round polymerase chain reaction primers flanking *cep-1* were 5'-GGTGGACTGTTGCTTTGAAATCAAGACTGC-3' and 5'-GCTCTTGATTTGCCAACAA-GATCGGATTC-3'. Second-round primers were 5'-CAGGGGAGTTGGCGTTAGG-3' and 5'-AATTGGTA-CAGCGACTTCTCTCA-3'. A single worm containing the *cep-1(w40)* deletion was identified. This deletion removes 1823 nucleotides of the gene, corresponding to nucleotides 28,754 to 31,967 on cosmid F52B5. The splice acceptor and donor sites remain intact in the *cep-1(w40)* allele, which is predicted to encode an in-frame but truncated protein missing amino acids 69 to 242. Further analysis showed that the deletion strain also carries an intact copy of *cep-1*. The *w40* allele segregates independently of the wild-type *cep-1* locus, indicating that the deleted copy had translocated to another region of the genome and a wild-type copy of *cep-1* remains at the normal locus.
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Integration Between the Epibranchial Placodes and the Hindbrain

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Developmental integration results from coordination among components of different embryonic fields to realize the later anatomical and functional relationships. We demonstrate that in the chick head, integration between the epibranchial placodes and the hindbrain is achieved as the neuroglial hindbrain crest cells guide the epibranchial neuronal cells inward to establish their central connections. This work defines a role for the neuroglial hindbrain crest in organizing the afferent innervation of the hindbrain.

After regional specification, during which constituent parts of an embryonic field are defined, the next developmental challenge is that of integration, during which the different embryonic fields are coordinated, and thus, later anatomy and function established. Developmental integration is particularly apparent in the vertebrate head, because head development involves integration of a number of disparate embryonic cell types (1). Here, we studied in the chick the development of the epibranchial ganglia: the geniculate, petrosal, and nodose, which convey gustatory and viscerosensory information from the oro-pharyngeal cavity to central sensory nuclei in the hindbrain (Fig. 1, A and B) (2). The sensory neurons of these ganglia originate in the epibranchial placodes and connect to the central nervous system (CNS) (3, 4). These placodes are focal thickenings of ectoderm close to the tips of the pharyngeal pouches, and which are induced by the pharyngeal endoderm through the action of Bmp-7 (5). It has been unclear, however, how the neuronal cells generated by the epibranchial placodes migrate internally to the site of ganglion formation. We show here that this process is mediated by the neuroglial rhombencephalic neural crest. The epi-

branchial neuronal cells move inward along the tracks of neuroglial neural crest that extend from the hindbrain to the placodes. These results define a role for the neuroglial hindbrain neural crest in the integration of hindbrain and epibranchial placode development.

With a view toward understanding this process, we characterized the migratory paths taken by the epibranchial placodal cells as they move internally. The placodal cells were labeled by application of the lipophilic dye DiI to the exterior of the embryo, at stages concomitant with the induction of these placodes (6). This procedure results in the labeling of the embryonic ectoderm. Cells that leave this tissue layer carry the label with them as they move inward (Fig. 1). Cells migrating from both the geniculate and the petrosal placodes form organized streams extending from the placodal ectoderm toward the hindbrain (Fig. 1).

The migratory paths formed by the epibranchial neuronal cells are reminiscent of those formed by another group of cells, the neural crest. The neural crest cells in this region of the embryo migrate as segregated streams from specific axial levels of the hindbrain (Fig. 2A) (7, 8). The crest cells within these streams, however, have two distinct fates. The early ventrally migrating population fill the underlying pharyngeal arches and form ectomesenchymal derivatives within these structures, whereas the

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